

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 13:02:26 ; Search time 41 Seconds

(without alignments)
1072.465 Million cell updates/sec

Title: US-10-654-428-2

Sequence: 1 MARRTEPPDGGWGVVLSA.....SLTAPGLLRLGLHRTVP 457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	% Match	Query Length	DB ID	Description
1	591	25.4	484	2	A55626
2	564	24.2	542	2	JC5507
3	555.5	23.8	494	2	A44458
4	546	23.4	494	2	JC4399
5	540	23.2	500	2	A55568
6	482.5	20.7	598	2	TJ32430
7	463.5	19.9	556	2	T16790
8	417.5	17.9	613	2	I39295
9	370.5	15.9	397	2	G69295
10	368.5	15.8	402	2	F95874
11	368.5	15.8	596	2	T23685
12	342	14.7	571	2	TJ3941
13	314.5	13.5	808	2	T16564
14	290.5	12.5	399	2	F83484
15	288	12.4	410	2	G82445
16	280	12.0	406	2	AG2704
17	290	12.0	414	2	G97486
18	250.5	10.7	407	2	AC1346
19	250.5	10.7	406	2	G69748
20	249.5	10.7	405	2	H81995
21	245.5	10.5	407	2	AF1716
22	245	10.5	418	2	F83986
23	241	10.3	426	2	T50944
24	238.5	10.2	402	2	S47768
25	236	10.1	673	2	S59263
26	233	10.0	400	2	H91182
27	233	10.0	400	2	D86029
28	232.5	10.0	400	2	T44249
29	229.5	9.8	431	2	AB2949

30	229.5	9.8	433	2	H98333	hypothetical prote
31	228.5	9.8	398	2	AD0828	probable transmem
32	226.5	9.7	430	2	S74039	hypothetical prote
33	226	9.7	473	2	S38065	hypothetical prote
34	225	9.7	444	2	E83033	probable MFS trans
35	222	9.5	419	2	H83965	hypothetical prote
36	220	9.4	420	2	H69250	oxalate/formate an
37	218	9.4	388	2	AG3307	oxalate/formate an
38	208	8.9	373	2	S00656	hypothetical prote
39	206	8.8	408	2	H95184	hypothetical prote
40	205	8.8	408	2	H98051	oxalate/formate an
41	201	8.6	412	2	T37042	major facilitator,
42	199.5	8.6	501	2	S66816	probable membrane
43	199.5	8.6	807	2	T20080	transport protein,
44	199.5	8.6	807	2	T20080	hypothetical prote
45	196.5	8.4	428	2	A75423	multidrug resistanc

ALIGNMENTS

RESULT 1

A55626
monocarboxylate transporter MCT2 - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 18-Sep-1998
C/Accession: A55626
R/Garcia, C.K.; Brown, M.S.; Patchak, R.K.; Goldstein, J.L.
J. Biol. Chem. 270, 1843-1849, 1995
A/Title: cDNA cloning of MCT2, a second monocarboxylate transporter expressed in differ
A/Reference number: A55626; MUID:9510566; PMID:7829520
A/Accession: A55626
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-484 <GMR>
A/Cross-references: UNIPARC:UP10000178E64; GB:D31957
C/Superfamily: monocarboxylate transporter MCT2
C/keywords: transmembrane protein

Query Match 25.4%; Score 591; DB 2; Length 484;
Best Local Similarity 33.1%; Pred. No. 9.7e-33;
Matches 135; Conservative 72; Mismatches 175; Indels 26; Gaps 4;

QY	7	PPDGGWGVVLSA	FPQSA	LVFGV	LSFGV	FEVFA	AEQAR	VS	WIAS	IGIA	VQDF	66
DB	14	PPDGGWGVVLSA	FPQSA	LVFGV	LSFGV	FEVFA	AEQAR	VS	WIAS	IGIA	VQDF	66
QY	67	SPVGSALSTKFG	PRPVVT	GTGIL	ALGML	ASFATS	SLTV	YIS	IGLS	SGMAL	TPAPLT	126
DB	74	GISSVLVNNVGS	RPVVI	IGIL	CTGMI	LSFSNS	VELT	ITL	PTIG	GLAFNI	QPAL	133
QY	127	ACTSCYFSRR	SLALG	ALTGV	GSST	FPFQML	LSHVM	KSG	SL	LVSA	LSLHVACG	186
DB	134	TTIGKYFR	RRPMNGL	MAGSP	FLSL	AFNQL	FNSY	GKKS	FL	LGIL	FLHSCVAG	193
QY	167	ALLRP	---	PSLA	DPVAG	GPRA	LT	---	---	---	---	223
DB	194	CLMPFVOTS	SPRKS	KSVK	SGVRS	QDGS	MKKAS	KSVT	AEKIN	FLDFS	LFKHGF	253
QY	224	TLVINTG	FIPFLH	VANL	QDLWD	PLPA	FLSV	VAIS	DLVGR	VSGWL	GDA--VP	281
DB	254	VIMPLG	FPATIF	FLAP	KXGVD	EVNALL	SVMA	LVDM	PAR	TGIL	ANSKIR	313
QY	282	RLMLMT	TLTGVS	IALP	PPVA	QAP	PA	VALA	VAG	FTSG	ALAFSV	341
DB	314	YFSP	FALV	GTGICH	LCLAD	TYPAL	VVTS	IFG	YGS	SVSVL	FETIM	373
QY	342	LGIL	QMTES	IGL	GLP	PLSG	YTL	RDVSG	NTAS	FPVAG	AFLLSG	389
DB	374	VGLAT	IVCC	PVLL	GPPL	AGK	IVDK	YKVM	YIAS	GI	TVI--SG	420

RESULT 2.

A:Molecule type: nucleic acid
A:Residues: 1-494 <KIM>
A:Cross-references: UNIPARC:UPI000017072E; GB:M97382; NID:g191143; PIDN:AAB59630.1; PID
A:Experimental source: CHO clone met-18b-2
A>Note: sequence extracted from NCBI backbone (NCBIP:118221)
R.Garcia, C.K.; Goldstein, J.L.; Pathak, R.K.; Anderson, R.G.W.; Brown, M.S.
Cell 76, 865-873, 1994
A>Title: Molecular characterization of a membrane transporter for lactate, pyruvate, and
A:Reference number: A49951; MOTID:94170387; PMID:8124722
A:Accession: J04399
A:Molecule type: mRNA
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 / 'F', 361-494 <RSS>
A:Cross-references: UNIPARC:PII000012F3BF; GB:L25842; NID:g472332; PIDN:AAB59731.1; PID
C:Superfamily: monocarboxylate transporter MCT2

Query Match 23.8%; Score 555.5; DB 2; Length 494;
Best Local Similarity 31.8%; Pred. No. 2.5e-30;
Matches 135; Conservative 64; Mismatches 182; Indels 43; Gaps 5;

QY 7 PPDGMEGVVVLISAFQSLAVFGVLRSFGVFVEFEVAEFEOAAARSWIASIGIAVOQG 66
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 13 PPDGMGWAVVVGAFISIGFSYAPPKSIVFEKEIEGINATTSSEWSISSIMLAWMYAG 72
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 67 SPVSALSTKEGPRPVVTMGILALGMLLASPATSLTHLYLSIGLLSGSMALTPEPTL 126
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 73 GPISSVLNKKSGRPVMTAGCLSCGGLIASFPCMTVCBELYLICIIVIGGLGFNLNPPL 132
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 127 ACISCYSRRRLATGTGLTGTGLSSFTFAPEFWMLSHYARGSLILVASLHVACG 186
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 133 TWICKTYKKRPLANGLAMASPVFLSTLPANQAFPGLFGWRGSPLLIGILLNCCVAG 192
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 187 ALLRP-----PSLAB-----DPVNGPRAQLTSLH----- 212
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 193 SLMRPIPKPGKTEKLKSKESLQEAKSEANTMDLGSPFKGRKRVLTQITNKFLDLSLA 252
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 213 HGPFIKRTVALTLINTGYFFPYLHLVAHLQDLDMDELPAPALLSVAISIDLGRVVSGWL 272
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 253 HRGPFLLYLSGNVWFPELFPLVPFLSNYGSKOHXSEKSAPELLSTLAFDVVARPSMGLA 312
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 273 GDA--VPGPYTRLIMLTTLTGVSIALFPYAQAFTALVALNAVYFTSGALAPLAFVTP 330
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 313 ANTKWIRPRIQFPFAPSVAANGCHLAPLUSTSYTGCTIVGVFGFACGMLSIVFETLM 372
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 331 ELIGTRITYCGLDLQIESIGLLGPPLSGYLDVSGNTYASF-----VVAGAFLIS 383
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 373 DLVGPORFSSAVGLVTVIECCPVLLGPPLGRLNDMGDYKYTWACGVIIILAITYLFI 432
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 384 GSGL 387
| | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 433 GMGI 436

RESULT 4
UC4399
monocarboxylate transporter - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: UC4399
R:Takanaga, H.; Tamai, I.; Inaba, S.; Sai, Y.; Higashida, H.; Yamamoto, H.; Tsuji, A.
Biochem. Biophys. Res. Commun. 217, 370-377, 1995
A>Title: cDNA cloning and functional characterization of rat intestinal monocarboxylate
A:Reference number: JC4399; MUID:96095680; PMID:852636
A:Accession: JC4399
A:Molecule type: mRNA
A:Residues: 1-494 <TK>
A:Cross-references: UNIPROT:P53987; UNIPARC:UPI000012F3C2; GB:D63834; NID:g119781; PID
A:Experimental source: Small intestinal mucosal cells
A:Genetics:
A:Gene: mct1
C:Superfamily: monocarboxylate transporter MCT2
C:Keywords: intestine; transmembrane protein; ...
C:16-36/Domain: Transmembrane #1

F:60-81/Domain: transmembrane #status predicted <TM2>
F:87-105/Domain: transmembrane #status predicted <TM3>
F:112-136/Domain: transmembrane #status predicted <TM4>
F:145-172/Domain: transmembrane #status predicted <TM5>
F:176-195/Domain: transmembrane #status predicted <TM6>
F:196-225/Region: hydrophilic
F:256-280/Domain: transmembrane #status predicted <TM7>
F:292-314/Domain: transmembrane #status predicted <TM8>
F:322-342/Domain: transmembrane #status predicted <TM9>
F:346-368/Domain: transmembrane #status predicted <TM10>
F:380-402/Domain: transmembrane #status predicted <TM11>
F:416-438/Domain: transmembrane #status predicted <TM12>

Query Match 23.4% Score 546; DB 2; Length 494;
Best Local Similarity 30.2%; Pred. No. 1,le-29;
Matches 145; Conservative 66; Mismatches 215; Indels 54; Gaps 7;

QY 7 PPDGKGRVVVLSAFQFQALVFGVLSFGVFFVFAAEQARVSWIASIGIAVOQFG 66
DB 13 PPDGKGRVVVLSAFQFQALVFGVLSFGVFFVFAAEQARVSWIASIGIAVOQFG 66
QY 67 SPVGSALSTKFGPRPVMTGGLAALGMLASFSATSLTHYLSIGLSGSMALTPAFTL 126
DB 73 GPISILVKNKSGRPVMTAGGCLSGCGLIASFCNTVOELVYICIGVIGGLAENLNPAL 132
QY 127 ACISCFYSRRSLATGALTGVLSSFTFAPFQWMLSHVAMRGSLLVLSLHVAAG 186
DB 133 TMIGKTFYKRRPLANGLAMAGSPVFLCTLAPLNQVFFGIFGWRGSLILGGLLNCVAG 192
QY 187 ALLRP-----PSLA-----DPAVGGPRAQ-----TSLLH 212
DB 193 SLMRPIPOQKVEKESKESLQAGKSDANTDILIGSPKESKSVQTNKFLDLSFT 252
QY 213 HGPFLRYTVALTLINTGYPIYLYLVAHLDLMDPLPAFLLSVAISLVGRVSGWL 272
DB 253 HREGLTLNNGVNVFGLFTPLVFLSNYKSKHPSSEKSAFLISILFVMMVAPRSMGLA 312
QY 273 GDA--VGPVTRLLMLTTLTGVSALFPVAQAPTLVALVAVGFSGALPLASVLP 330
DB 313 ANRWIRPRQYPPASVAVANGVCHLAPLSTTYVGCITAGVGFAGMLSVLEFTLM 372
QY 331 ELIGTRIRYIGLGLQMTESIGLGPPLSGYLVDVSGNYTASF-----VVAQAFILS 383
DB 373 DLVGPRFSSAVGLVTVCCPVLGLPPLGRLNDMGDKYTYMAGVLLIAGLYLFI 432
QY 384 GSGI--LTLPHFCSTTSSGPODVTALD-----TVPLPKKGLKGLNSTES 432
DB 433 GNGINRYLVAKEQAKKEDKEDSTVDDEKPKTKMETQSPAPLQNSGDPAREES 492

RESULT 5
A:Accession: A55568
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
R:Garcia, C.K.; Li, X.; Luna, J.; Francke, U.
Genomics 23, 500-503, 1994
A:Title: CDNA Cloning of the human monocarboxylate transporter 1 and chromosomal localization
A:Reference number: A55568; MUID:95137602; PMID:7835905
A:Accession: A55568
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-500 <GAR>
A:Cross-references: UNIPROT:P53985; UNIPARC:UP1000016ADB; GB:I31801; NID:9561721; PIDN:
A:Note: authors translated the codon GCA for residue 279 as Asp
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224379
A:Accession: T47157
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-479, 'A', 481-500 <AAA>

A:Cross-references: UNIPARC:UP1000012F3C0; EMBL:AL162079
A:Experimental source: adult melanoma (Memo cell line); clone DKFZp762B2310
C:Genetics:
A:Gene: GDB:SLC16A1; MCT
A:Gene: GDB:373211; OMIM:600682
A:Map position: 1p13.2-1p12
A:Note: DKFZp762B2310-1
C:Superfamily: monocarboxylate transporter MCT2

Query Match 23.2% Score 540; DB 2; Length 500;
Best Local Similarity 30.6%; Pred. No. 2,8e-29;
Matches 133; Conservative 64; Mismatches 181; Indels 56; Gaps 6;

QY 7 PPDGKGRVVVLSAFQFQALVFGVLSFGVFFVFAAEQARVSWIASIGIAVOQFG 66
DB 13 PPDGKGRVVVLSAFQFQALVFGVLSFGVFFVFAAEQARVSWIASIGIAVOQFG 66
QY 67 SPVGSALSTKFGPRPVMTGGLAALGMLASFSATSLTHYLSIGLSGSMALTPAFTL 126
DB 73 GPISILVKNKSGRPVMTAGGCLSGCGLIASFCNTVOELVYICIGVIGGLAENLNPAL 132
QY 127 ACISCFYSRRSLATGALTGVLSSFTFAPFQWMLSHVAMRGSLLVLSLHVAAG 186
DB 133 TMIGKTFYKRRPLANGLAMAGSPVFLCTLAPLNQVFFGIFGWRGSLILGGLLNCVAG 192
QY 187 ALLRPSLAEDPAVGG-----PRAQ----- 206
DB 193 ALMRP--IGPKPTKAGDKSKASLEKAGSGYKDLHDANTDILGHPKQEKSVPTIN 250
QY 207 ----LTLNHPFLRYTVALTLINTGYPIYLYLVAHLDLMDPLPAFLLSVAISD 262
DB 251 QELDLTLFTHRG-FLLYLSGNVIMFFGLFAPLVFLSSYSKSHYSEKSAFLISILAFVD 309
QY 263 LVGRVVSGLDPAV--GPVTRLLMLTTLTGVSALFPVAQAPTLVALVAVGFSGA 320
DB 310 MVAREPMGVANTKPRIRPIQYPPASVAVANGVCHLAPLSTTYVGCITAGVGFAG 369
QY 321 LAPLAFSVLELIGTRIRYIGLGLQMTESIGLGPPLSGYLVDVSGNYTASF----- 374
DB 370 LSSVLFETLMDLVGPRFSSAVGLVTVCCPVLGLPPLGRLNDMGDKYTYMAGV 429
QY 375 -VVAQAFILSGSI 387
DB 430 ILISGTYLFIGMI 443

RESULT 6
T32430
Hypothetical protein C10E2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
R:Wohlmann, P.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid C10E2.
A:Reference number: Z21165
A:Accession: T32430
A:Status: Preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-598 <NOH>
A:Cross-references: UNIPROT:O17328; UNIPARC:UP1000017B768; EMBL:AF026202; PIDN:AA871245
A:Experimental source: strain Bristol N2; clone C10E2
C:Genetics:
A:Gene: CESP:C10E2.6
A:Map position: X
A:Introns: 53/3; 103/2; 145/2; 476/3; 569/3
Query Match 20.7% Score 482.5; DB 2; Length 598;
Best Local Similarity 23.4%; Pred. No. 2,6e-25;
Matches 135; Conservative 75; Mismatches 181; Indels 185; Gaps 8;
QY 7 PPDGKGRVVVLSAFQFQALVFGVLSFGVFFVFAAEQARVSWIASIGIAVOQFG 66

GenCore version 5.1.9
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3M protein - protein search, using sw model

Run on: September 7, 2006, 12:59:01 ; Search time 301 Seconds

(without alignments)
1404.426 Million cell updates/sec

Title: US-10-654-428-2

Perfect score: 2331

Sequence: 1 MARRTEPPDGGWGRVVLASA.....SLTAPGLLRLGLHRTTP 457

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 segs, 925015592 residues

total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 7.2.*
1: UniProt_sprot.*
2: UniProt_trmb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sult No.	Score	Query Match	Length	ID	Description
1	2151	92.3	426	2 Q7RYO_HUMAN	Q7RYO homo sapien
2	2142	91.9	424	2 Q2VP92_HUMAN	Q2VP92 homo sapien
3	1899.5	81.5	428	2 Q6GHE2_RAT	Q6GHE2 rattus norv
4	1888.5	81.0	428	2 Q8CE94_MOUSE	Q8CE94 mus musculu
5	1861.5	79.9	428	2 Q8CEH6_MOUSE	Q8CEH6 mus musculu
6	1441.5	61.8	335	2 Q8CF46_MOUSE	Q8CF46 mus musculu
7	1068.5	45.8	519	2 Q5MTD0_XENLA	Q5MTD0 xenopus lae
8	938.5	40.3	447	2 Q5NCG2_MOUSE	Q5NCG2 mus musculu
9	930.5	39.9	471	2 Q8NCK7_HUMAN	Q8NCK7 homo sapien
10	688	29.5	433	2 Q4KX10_HUMAN	Q4KX10 xenopus lae
11	664.5	28.5	533	2 Q8O1R0_XENLA	Q8O1R0 brachydanio
12	645	27.7	492	1 MOT3_RAT	Q70461 rattus norv
13	643	27.6	290	2 Q9JJC0_MOUSE	Q9JJC0 mus musculu
14	640	27.5	486	2 Q8BGC3_MOUSE	Q8BGC3 m 14, 17 da
15	637.5	27.2	463	2 Q5T7J2_HUMAN	Q5T7J2 homo sapien
16	634.5	27.2	486	2 Q6ZSM3_HUMAN	Q6ZSM3 homo sapien
17	632	27.1	460	2 Q6GMS9_XENLA	Q6GMS9 xenopus lae
18	632	27.1	492	2 Q5O3M4_BRARE	Q5O3M4 brachydanio
19	631	27.1	492	1 MOT3_MOUSE	Q53308 mus musculu
20	631	27.1	492	1 Q5UB50_MOUSE	Q5UB50 mus musculu
21	629.5	27.0	504	2 MOT3_HUMAN	Q5BDS0 mus musculu
22	624.5	26.8	473	2 Q6P2X9_XENTR	Q6P2X9 homo sapien
23	620	26.6	489	2 Q6GHS9_RAT	Q6GHS9 xenopus tiro
24	617	26.5	489	1 MOT2_RAT	Q63344 rattus norv
25	609	26.1	484	1 MOT2_MOUSE	Q70451 mus musculu
26	608.5	26.1	435	1 Q5RFH2_PONPY	Q5RFH2 pongo pygma
27	608	26.1	478	1 MOT2_HUMAN	Q60669 homo sapien
28	607.5	26.1	523	2 Q3TCV8_MOUSE	Q3TCV8 mus musculu
29	607.5	26.0	523	2 Q91W47_MOUSE	Q91W47 mus musculu
30	606.5	26.0	607	2 Q8C086_MOUSE	Q8C086 mus musculu
31	605.5	26.0	478	2 Q8NEM3_HUMAN	Q8NEM3 homo sapien

32	603.5	25.9	465	2 Q5RDA0_PONPY	Q5RDA0 pongo pygma
33	601	25.8	484	2 Q4FK61_MOUSE	Q4FK61 mus musculu
34	600.5	25.8	523	2 Q6PIX3_HUMAN	Q6PIX3 homo sapien
35	599.5	25.7	523	1 MOT7_HUMAN	Q15403 homo sapien
36	599	25.7	522	2 Q7TMR7_RAT	Q7TMR7 rattus norv
37	595	25.5	484	1 MOT2_MESAU	Q53588 mesocricetu
38	594.5	25.5	428	2 Q4S087_TETNG	Q4S087 tetraodon n
39	591.5	25.4	465	1 MOT4_HUMAN	Q15427 homo sapien
40	591.5	25.4	465	2 Q4S087_TETNG	Q4S087 homo sapien
41	591.5	25.4	465	2 Q2M1P8_HUMAN	Q2M1P8 homo sapien
42	583	25.0	472	2 Q6GMS9_XENLA	Q6GMS9 xenopus lae
43	581	24.9	470	1 MOT4_MOUSE	Q51787 mus musculu
44	581	24.9	470	1 Q3UDP9_MOUSE	Q3UDP9 m bone marr
45	579.5	24.9	471	1 MOT4_RAT	Q35810 rattus norv

ALIGNMENTS

RESULT 1
Q7RYO_HUMAN PRELIMINARY; PRT; 426 AA.
ID Q7RYO;
AC Q7RYO;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Monocarboxylate transporter 13.
GN Name=SLC16A13;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hallestap A.P.; Meredith D.;
RT "The SLC16 gene family - from monocarboxylate transporters (MCTs) to
RL aromatic amino acid transporters and beyond.";
RL Plingers Arch. 0:0-0(0).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Hallestap A.P.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-1- MISCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DDBJ third party annotation (TPA) entry.
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CC License
CC EMBL; BN000145; CAD80156.1; -; mRNA.
CC EMBL; ENSG00000174337; Homo sapiens.
CC DR HGNC; HGNC:31037; SLC16A13.
CC DR GO; GO:0016021; C:integral to membrane; IEA.
CC DR GO; GO:0016020; C:membrane; IEA.
CC DR GO; GO:0005215; F:transporter activity; IEA.
CC DR GO; GO:0006810; P:transport; IEA.
CC DR InterPro; IPR007114; MFS.
CC DR Pfam; PF07690; MFS_1; 1.
CC DR PROSITE; PS50850; MFS; 1.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 426 AA; 44992 MW; 6A6849507C933624 CRC64;
Query Match 92.3%; Score 2151; DB 2; Length 426;
Best Local Similarity 99.5%; Pred. No. 3,9e-143;
Matches 422; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MARRTEPPDGGWGRVVLASAFQSLVFGVLSFGVFVFAAREQARVSWIASIGI 60
DB 1 MARRTEPPDGGWGRVVLASAFQSLVFGVLSFGVFVFAAREQARVSWIASIGI 60
QY 61 AVOQGSVGSALSTKRPGRPVVMTGGTIALGMLASFASTLTLYLSIGLSSGNAL 120

Appendix B

Db 61 AVQGGSPVGSALSTLNKFEPRRVVMTGGIILALQMLIASPSTLTHLYSLIGLSSGGMAL 120

Qy 121 TRAPFLIACISCFSPRRSLATGALTGVGLSPFPAPFFQMLLSHYAMRGSLIVSALSL 100

Db 121 TRAPFLIACISCFSPRRSLATGALTGVGLSPFPAPFFQMLLSHYAMRGSLIVSALSL 180

Qy 181 HVAAGCALLRPPSLAEPPAVGGPRAOUTSLHHGPRLRTVALTLINTGYTPYLHVH 240

Db 181 HVAAGCALLRPPSLAEPPAVGGPRAOUTSLHHGPRLRTVALTLINTGYTPYLHVH 240

Qy 241 LODLDMDPLPAAPFLLSVAASIDLVGVSGWGLGDAPGVYRILMLMTTLTGVSLAPV 300

Db 241 LODLDMDPLPAAPFLLSVAASIDLVGVSGWGLGDAPGVYRILMLMTTLTGVSLAPV 300

Qy 301 AOAFLVALVALVAVAGFSGALAPLASVPELIGTRIRYICGLGLQWIESIGLIGPPLS 360

Db 301 AOAFLVALVALVAVAGFSGALAPLASVPELIGTRIRYICGLGLQWIESIGLIGPPLS 360

Qy 361 GTLDVSGNVTASFPVAGAFILSGSIIITLPHFCSTTTSSGGQDVTALTKYPLPK 420

Db 361 GTLDVSGNVTASFPVAGAFILSGSIIITLPHFCSTTTSSGGQDVTALTKYPLPK 420

Qy 421 EGLE 424

Db 421 EGLE 424

RESULT 2

QY:FE92 HUMAN

DB:02VP92 HUMAN PRELIMINARY, PRT: 424 AA.

DB:02VP92

DB:10-JAN-2006 Integrated into UniProtKB/TrEMBL.

DB:10-JAN-2006, sequence version 1.

DB:07-FEB-2006, entry version 3.

SLC16A13 protein (Fragment).

QY: Name=SLC16A13;

DB: Name=SLC16A13;

QY: Homo sapiens (Human).

DB: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DB: Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

DB: NCBI_TaxID=9606;

DB: (1)

NCBIEOTIDE SEQUENCE.

RE TISSUE=PCR rescued clones.

RE MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603999;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg H., Buetow K.H., Scheffer C.F., Bat N.K., Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Umed T.B., Toshiyuki S., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulik S.W., Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A., Faneley J., Helton E., Kettelman M., Mada A., Rodriguez A.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalls D.E., Scherach A., Schein J.E., Jones S.J.M., Maria M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

NCBIEOTIDE SEQUENCE.

P: TISSUE=PCR rescued clones;

G: NIH MGC Project;

U: Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.

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Query Match	Best Local Similarity	Score	DB 2	Length
91.9%;	99.5%;	2142;	DB 2;	Length 434;
Matches 420;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps
Query	3	RTPEPPDGMGVVVLASAFQSAALFVGLRSGVFVEVVAPEBOA	VSMIASIGLV	62
Db	1	RTPEPPDGMGVVVLASAFQSAALFVGLRSGVFVEVVAPEBOA	VSMIASIGLV	60
Query	63	QOPGSPVSGALSTKRGPRPVVWTGGIILALGMLASFATSLTHLYLS	GLISGSGMALTF	12
Db	61	QOPGSPVSGALSTKRGPRPVVWTGGIILALGMLASFATSLTHLYLS	GLISGSGMALTF	12
Query	122	APTALACISCFPSRRSLATGTLATGVLGSSSTFPAPFQMLSHYAMRSL	LLVSAALSLHL	18
Db	121	APTALACISCFPSRRSLATGTLATGVLGSSSTFPAPFQMLSHYAMRSL	LLVSAALSLHL	18
Query	183	VACGALLRPSPALSDPAVGPRAQUTSLHHGPELRVVALTLINTGY	TPYHLVAHQ	24
Db	181	VACGALLRPSPALSDPAVGPRAQUTSLHHGPELRVVALTLINTGY	TPYHLVAHQ	24
Query	243	DIDMDPLPAFLLSVVAISDLVGRVSGMLGDAVAGPVTRLMLMTIT	TGYSIALFPVQ	30
Db	241	DIDMDPLPAFLLSVVAISDLVGRVSGMLGDAVAGPVTRLMLMTIT	TGYSIALFPVQ	30
Query	303	APTALVLAAYVYGTSGALAPLASVPELIGTRIRYVGLLQMLER	IGLIGPPLSGY	36
Db	301	APTALVLAAYVYGTSGALAPLASVPELIGTRIRYVGLLQMLER	IGLIGPPLSGY	36
Query	363	LRDVSGNYTASFVAAGFLLSGGILLTPHPFCSTTSSGGPODLVT	EAADTVPLPKKG	42
Db	361	LRDVSGNYTASFVAAGFLLSGGILLTPHPFCSTTSSGGPODLVT	EAADTVPLPKKG	42
Query	423	LE 424		
Db	421	LE 422		

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:59:01 ; Search time 301 Seconds
(without alignments)
1404.426 Million cell updates/sec

Title: US-10-654-428-2
Perfect score: 2331
Sequence: 1 MARRTEPPDGGWGRVVLSA.....SLTAPGLLPLRLGHTTVP 457

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2151	92.3	426	Q7RYO_HUMAN	Q7RYO homo sapien
2	2142	91.9	424	Q2VP2_HUMAN	Q2VP2 homo sapien
3	1899.5	81.5	428	Q66H2_RAT	Q66H2 rattus norv
4	1888.5	81.0	428	Q8CE94_MOUSE	Q8CE94 mus musculu
5	1861.5	79.9	428	Q8CEH6_MOUSE	Q8CEH6 mus musculu
6	1441.5	61.8	335	Q8CF46_MOUSE	Q8CF46 mus musculu
7	1068.5	45.8	519	Q5MTD0_XENLA	Q5MTD0 xenopus lae
8	938.5	40.3	447	Q5NCJ2_MOUSE	Q5NCJ2 mus musculu
9	930.5	39.9	471	Q8NCK7_HUMAN	Q8NCK7 homo sapien
10	668	29.5	433	Q4XN10_BRARE	Q4XN10 brachydanio
11	664.5	28.5	533	Q801R0_XENLA	Q801R0 xenopus lae
12	645	27.7	492	MOT3_RAT	MOT3 rattus norv
13	643	27.6	290	Q9JIC0_MOUSE	Q9JIC0 mus musculu
14	640	27.5	486	Q8BGC3_MOUSE	Q8BGC3 m 14, 17 da
15	637.5	27.3	463	Q5TJ2_HUMAN	Q5TJ2 homo sapien
16	634.5	27.2	486	Q6ZSM3_HUMAN	Q6ZSM3 homo sapien
17	632	27.1	460	Q6GM59_XENLA	Q6GM59 xenopus lae
18	632	27.1	477	Q5O3M4_BRARE	Q5O3M4 brachydanio
19	631	27.1	492	MOT3_MOUSE	MOT3 mus musculu
20	629.5	27.0	504	Q5UB50_MOUSE	Q5UB50 mus musculu
21	629.5	26.8	473	MOT3_HUMAN	MOT3 homo sapien
22	624.5	26.8	473	Q6P2X9_XENTR	Q6P2X9 xenopus tiro
23	620	26.6	489	Q6BHS9_RAT	Q6BHS9 rattus norv
24	617	26.5	489	MOT2_RAT	MOT2 rattus norv
25	609	26.1	484	MOT2_MOUSE	MOT2 mus musculu
26	608.5	26.1	435	Q5RPH2_PONPY	Q5RPH2 pongo pygma
27	608	26.1	478	MOT2_HUMAN	MOT2 homo sapien
28	607.5	26.1	523	Q3TCY8_MOUSE	Q3TCY8 mus musculu
29	607.5	26.1	523	Q91W47_MOUSE	Q91W47 mus musculu
30	606.5	26.0	607	Q8C086_MOUSE	Q8C086 mus musculu
31	605.5	26.0	476	Q8NEM3_HUMAN	Q8NEM3 homo sapien

32	603.5	25.9	465	Q5RDA0_PONPY	Q5RDA0 pongo pygma
33	601	25.8	484	Q4FK61_MOUSE	Q4FK61 mus musculu
34	600.5	25.8	523	Q6PIX3_HUMAN	Q6PIX3 homo sapien
35	599.5	25.7	523	MOT7_HUMAN	MOT7 homo sapien
36	599	25.7	522	Q7TMR7_RAT	Q7TMR7 rattus norv
37	595	25.5	484	MOT2_MESAU	MOT2 mesocricetu
38	594.5	25.5	428	Q4S087_TETNG	Q4S087 tetradodon n
39	591.5	25.4	465	MOT4_HUMAN	MOT4 homo sapien
40	591.5	25.4	465	Q53G91_HUMAN	Q53G91 homo sapien
41	591.5	25.4	465	Q2M1P8_HUMAN	Q2M1P8 homo sapien
42	583	25.0	472	Q6GM98_XENLA	Q6GM98 xenopus lae
43	581	24.9	470	MOT4_MOUSE	MOT4 mus musculu
44	581	24.9	470	Q3UDP9_MOUSE	Q3UDP9 mus musculu
45	579.5	24.9	471	MOT4_RAT	MOT4 rattus norv

ALIGNMENTS

RESULT 1

ID	Q7RYO_HUMAN	PRELIMINARY;	PRT;	426 AA.
AC	Q7RYO;			
DT	15-DEC-2003;	Integrated into UniProtKB/TrEMBL.		
DT	15-DEC-2003;	sequence version 1.		
DT	07-FEB-2006;	entry version 14.		
DE	Monocarboxylate transporter 13.			
GN	Name=SLC16A13;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RA	NCLEOTIDE SEQUENCE.			
RA	Haestrap A.P.; Meredith D.;			
RT	"The SLC16 gene family - from monocarboxylate transporters (MCTs) to aromatic amino acid transporters and beyond.";			
RL	Pflegers Arch. 0:0-0(0).			
RN	[2]			
RA	NCLEOTIDE SEQUENCE.			
RA	Haestrap A.P.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DBJ third party annotation (TPA) entry.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs license			
DR	EMBL; BN000145; CAD80156.1; -; mRNA.			
DR	Ensembl; ENSG00000174327; Homo sapiens.			
DR	GENC; HSNC:31037; SLC16A13.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005215; F:transporter activity; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR011701; MFS_1.			
DR	InterPro; IPR011701; MFS_1.			
DR	PFam; PF07690; MFS_1; 1.			
DR	PROSITE; PS00850; MFS; 1.			
KW	Membrane; Transmembrane; Transport.			
SC	SEQUENCE 426 AA; 44992 MW; 6A6849507C933624 CRC64;			
Query Match	92.3%;	Score 2151;	DB 2;	Length 426;
Best Local Similarity	99.5%;	Pred. No. 3.9e-143;		
Matches 422;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 MARRTEPPDGGWGRVVLSAFPOSALVFGVLSFGVFEPVAAFEQAAVSWIASIGI 60			
DB	1 MARRTEPPDGGWGRVVLSAFPOSALVFGVLSFGVFEPVAAFEQAAVSWIASIGI 60			
QY	61 AVOGSGSPVGSALSTKRPFRPVYMGILALGMLASATSLTHLYSIGLLSGMAL 120			

Db 61 AVQFGSPVGSALSTKGPFPVMTGGIILAAAGMLASFAISLTHLYSLIGLSSGSMAL 120
QY 121 TFAPTLACISCFYRRRSRLATGALTGVGLSSFTFAFPQWMLSHYAMRGSLLVLSALSI 180
FT 121 TFAPTLACISCFYRRRSRLATGALTGVGLSSFTFAFPQWMLSHYAMRGSLLVLSALSI 180
Db 181 HLVAACGALLRPSPSLADPPAVGPPRAQLTSLHHGPFRLRYVALTLINTGYFIPYLHLVAH 240
QY 181 HLVAACGALLRPSPSLADPPAVGPPRAQLTSLHHGPFRLRYVALTLINTGYFIPYLHLVAH 240
Db 181 HLVAACGALLRPSPSLADPPAVGPPRAQLTSLHHGPFRLRYVALTLINTGYFIPYLHLVAH 240
QY 241 LQDLDMDPLPAAPFLLSVAISDLVGRVVGWLGDAVGPVTRLLMTTTLTGVSIALFPV 300
Db 241 LQDLDMDPLPAAPFLLSVAISDLVGRVVGWLGDAVGPVTRLLMTTTLTGVSIALFPV 300
QY 301 AQAFTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILGLOMIESIGLGPPLS 360
Db 301 AQAFTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILGLOMIESIGLGPPLS 360
QY 361 GYLADVSGNNTASRVVAGAFLLSSGILLTLPHFFCSTTTSQPDVTEALDTKVPPLK 420
Db 361 GYLADVSGNNTASRVVAGAFLLSSGILLTLPHFFCSTTTSQPDVTEALDTKVPPLK 420
QY 421 EGLE 424
Db 421 EGLE 424
RESULT 2
Q2VP92 HUMAN PRELIMINARY; PRT; 424 AA.
AC Q2VP92
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE SL16A13 protein (Fragment).
GN Name=SL16A13;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schmechel A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RN NHG MGC Project;
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL: BC109286; AA109287.1; -, mRNA.
DR EMBL; BC109286; AA109287.1; -, mRNA.
FT NON-TER 1
SQ SEQUENCE 424 AA; 44789 MW; 9146D21BC6310E39 CRC64;
Query Match 91.9%; Score 2142; DB 2; Length 424;
Best Local Similarity 99.5%; Pred. No. 1.7e-142;
Matches 420; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 RTEPPDGGKGRVVVLSAFQSGALVGVLRSGVFVEVPAFAFEQOARVSIASIGLAV 62
Db 1 RTEPPDGGKGRVVVLSAFQSGALVGVLRSGVFVEVPAFAFEQOARVSIASIGLAV 60
QY 63 QOFGSPVGSALSTKGPFPVMTGGIILAAAGMLASFAISLTHLYSLIGLSSGSMALNF 122
Db 63 QOFGSPVGSALSTKGPFPVMTGGIILAAAGMLASFAISLTHLYSLIGLSSGSMALNF 120
QY 123 APTLACISCFYRRRSRLATGALTGVGLSSFTFAFPQWMLSHYAMRGSLLVLSALSIH 182
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QY 183 VACGALLRPSPSLADPPAVGPPRAQLTSLHHGPFRLRYVALTLINTGYFIPYLHLVAHQ 242
Db 183 VACGALLRPSPSLADPPAVGPPRAQLTSLHHGPFRLRYVALTLINTGYFIPYLHLVAHQ 240
QY 243 LQDMDPLPAAPFLLSVAISDLVGRVVGWLGDAVGPVTRLLMTTTLTGVSIALFPVAQ 302
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QY 303 APTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILGLOMIESIGLGPPLSGY 362
Db 303 APTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILGLOMIESIGLGPPLSGY 360
QY 361 LRDVNTGYTASRVVAGAFLLSSGILLTLPHFFCSTTTSQPDVTEALDTKVPPLK 420
Db 361 LRDVNTGYTASRVVAGAFLLSSGILLTLPHFFCSTTTSQPDVTEALDTKVPPLK 420
QY 423 LE 424
Db 423 LE 424
RESULT 3
O66HE2 RAT PRELIMINARY; PRT; 428 AA.
ID O66HE2 RAT
AC O66HE2;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Solute carrier family 16 (monocarboxylic acid transporters), member 13.
GN Name=SL16A13;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney.
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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Blake J.A., Brack D., Bruscia V., Choithia C., Corbani L.E., Cousins S.,
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Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grumond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kani A., Kawaji H., Kawasawa Y., Kedierski R.M., King B.L.,
Kang A.A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenize L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.D., Petrea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
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60,770 full-length cDNAs";
Nature 420:563-573 (2002).
[5]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
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Nature 409:685-690 (2001).
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NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
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prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
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NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Skin;
MEDLINE=20530933; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwaga K.,
Fujisaki S., Inoue K., Togawa K., Izawa M., Otsuka E., Watanabe K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura T., Kawai J.,
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RT "RIKEN integrated sequence analysis (RISA) system-364-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[8]
NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
ADACHI J., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Fukuda S., Kawai J., Kondo S., Kono H., Kouda M., Koya S.,
Kuroh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
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Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
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Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[9]
NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Salivary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strasberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Ustin T.B., Toshitsugu S., Carninci P., Prange C.,
Rah S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.W.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[10]
NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Salivary gland;
RC Director MGC Project;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
[11]
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RA Sycamore N.,
Query Match 81.0%; Score 1888.5; DB 2; Length 428;
Best Local Similarity 87.0%; Pred. No. 1,2e-124;
Matches 367; Conservative 24; Mismatches 30; Indels 1; Gaps 1;
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X 1 MVRRAEPDGGGMMVVLIAFFQSAALVFGVLRSGVFVEVAAFEEDQARVSAISGI 60
DB 1 MVRRAEPDGGGMMVVLIAFFQSAALVFGVLRSGVFVEVAAFEEDQARVSAISGI 60
QY 61 AVQGGSVGASLSTKPGRPVMTGGTALAGMLASFATSLTHLYSIGLSSGVAL 120
DB 61 AVQGGSVGASLSTKPGRPVMTGGTALAGMLASFATSLTHLYSIGLSSGVAL 120
QY 121 TPAFTLACLSYPSRRSLATGLATVGLSSFTPAFFQWLSHYAARGSLTVALSL 180
DB 121 TPAFTLACLSYPSRRSLATGLATVGLSSFTPAFFQWLSHYAARGSLTVALSL 180
QY 161 HLVAAGALLRPPLAEDAVGAPPAQLTSLHHGPFLELYTVALTLINNGYFIPYHLVAH 240
DB 161 HLVAAGALLRPPLAEDAVGAPPAQLTSLHHGPFLELYTVALTLINNGYFIPYHLVAH 240
QY 241 LODLDMDPLPAFLISVAISDLVGRVVGWLDGAVPQVTRRLMLMTTLTGVSLALRPV 300

Db 241 LODLMDPLPAFLSLVAASVLDVGRVAGMLGDVAGPFAILLMLMTLLTGVSIALPFPV 300
 Qy 301 AQAFTALVALAVAGFTSGALAPLAFSVLPETLIGTRIRICGHLQMIESTIGLGPPLS 360
 Db 301 AQAASSTLVLAAYAGFTSGALPFAVSVLPVETLIGTRICGHLQMIESTIGLGPPLS 360
 2y 361 GYLPRVSGNYTASFYVAGAFLLSGGILITLPHFF-CESTTTSGPDVLVTEALDTKVPPL 419
 Db 361 GYLPRVSGNYTASFYVAGAFLLSGGILITLPHFFSCISVSTSPQDLVTEASDTKILPL 420
 2y 420 KE 421
 Db 421 KE 422
 RESULT 5
 28CEH6_MOUSE PRELIMINARY: PRT: 428 AA.
 1C 08CEH6_MOUSE
 1T 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 1T 01-MAR-2003, sequence version 1.
 1T 07-FEB-2006, entry version 20.
 1E Adult male tongue cDNA, RIKEN full-length enriched library,
 1E clone:23100003j18 product:RIKEN cDNA 1700007D07.
 1N Name=Slc16a13;
 1S Mus musculus (Mouse).
 1S Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1C Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 1C Muridae; Muridae; Murinae; Mus.
 1X NCBI_TaxID=10090;
 1P NUCLEOTIDE SEQUENCE.
 1P STRAIN=C57BL/6J; TISSUE=Tongue;
 1P MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 1A Carninci P., Hayashizaki Y.,
 1A Carninci P., Hayashizaki Y.,
 1L High-efficiency full-length cDNA cloning. ;
 1L Methods Enzymol. 303:19-44(1999).
 1L (2)
 1P NUCLEOTIDE SEQUENCE.
 1P STRAIN=C57BL/6J; TISSUE=Tongue;
 1P PubMed=16141072; DOI=10.1126/science.1112014;
 1A Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 1A Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 1A Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 1A Davis M.J., Wilm M., Dalrymple L.G., Ashwin V., Allen J.E.,
 1A Ambesi-Impomato A., Apweiler R., Attalaya R.N., Baileij T.L.,
 1A Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 1A Chiu K.P., Chowdhury V., Christoffels A., Clutterbuck D.R.,
 1A Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 1A di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 1A Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
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 1A Hill D., Hummelbeck J., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 1A Jakt M., Kanapin A., Karcch M., Kawasawa Y., Kelso A., Kitamura H.,
 1A Kiteano H., Koillies G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 1A Kurochkin I.V., Larau L.F., Lazarevic D., Lipovich L., Liu J.,
 1A Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 1A Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 1A Mottacchi-Fabber S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 1A Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 1A Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pelosi G.,
 1A Petrovski Y., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
 1A Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 1A Schonbach C., Sekiguchi K., Semple C.A., Sengo S., Seesla B., Sheng Y.,
 1A Shibata Y., Shimada H., Shimada C., Silva D., Sinclair B.,
 1A Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 1A Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 1A Terauchi H., Van Nimegen E., Verardo R., Wei C.L., Yagi K.,
 1A Yamashita H., Zabarovsky E., Zharov S., Zimmer A., Hilde W., Bult C.,
 1A Glimond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 1A Mahlestedt C., Matlick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
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 1A Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimomiya N.,
 1A Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 1A Tagami M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 1A Hayashizaki Y.,
 1R "The transcriptional landscape of the mammalian genome.",
 1R Science 309:1559-1563(2005).
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 1P NUCLEOTIDE SEQUENCE.
 1P STRAIN=C57BL/6J; TISSUE=Tongue;
 1P PubMed=16441073; DOI=10.1126/science.1112009;
 1R RIKEN Genome Exploration Research Group, and Genome Science Group
 1R (Genome Network Core team) and the FANTOM Consortium;
 1R "Antisense transcription in the mammalian transcriptome.",
 1R Science 309:1564-1566(2005).
 1R [4]
 1P NUCLEOTIDE SEQUENCE.
 1P STRAIN=C57BL/6J; TISSUE=Tongue;
 1P MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 1R Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 1R Nakai I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
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 1R Blake J.A., Brad D., Brusic V., Chothia C., Corbett L.E., Cousins S.,
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 1R Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
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 1R Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pelosi G.,
 1R Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 1R Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 1R Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 1R Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 1R Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 1R Wilm M., Wilmshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
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 1R Hirizane-Kishikawa T., Kono H., Nakamura M., Sakakura N.,
 1R Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuoka S.,
 1R Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kikawa I.,
 1R Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 1R Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 1R Birney E., Hayashizaki Y.,
 1R "Analysis of the mouse transcriptome based on functional annotation of
 1R 60,770 full-length cDNAs.",
 1R Nature 420:563-573(2002).
 1R [5]
 1P NUCLEOTIDE SEQUENCE.
 1P STRAIN=C57BL/6J; TISSUE=Tongue;
 1P MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 1R Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 1R Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuoka S.,
 1R Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 1R Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 1R Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 1R Flicschman N., Gaasterland T., Gissi C., King B., Kochava H.,
 1R Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pelosi G., Quackenbush J.,
 1R Schirral L.M., Steadly F., Suzuki R., Tomita M., Wagner L., Washio T.,
 1R Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barih G.,
 1R Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 1R Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
 1R Lyons P., Marchionni L., Mashima M., Hume D.A., Kamiya M., Lee N.H.,
 1R Nordone P., Ring B., Ringwald M., Mazzarelli J., Monbaerts P.,
 1R Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 1R Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
 1R Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 1R Hayashizaki Y.,
 1R "Functional annotation of a full-length mouse cDNA collection.",
 1R Nature 409:685-690(2001).
 1R [6]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Tongue; MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 Genome Res. 10:1617-1630(2000).
 [7]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Tongue; MEDLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 Genome Res. 10:1757-1771(2000).
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NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Tongue; Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohshio M., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.

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EMBL: AK028143; BAC25771.1; -; mRNA.

Ensembl: ENSMUSG0000044367; Mus musculus.

MG1; MG1:1916559; S1C16A13.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005215; P:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro: IPR007114; MPS.

InterPro: IPR011701; MPS_1.

Pfam: PF07690; MPS_1.1.

PROSITE: PS50850; MPS; 1.

Membrane; Transmembrane; Transport.

SEQUENCE 428 AA; 44878 MW; 83CF037FA0407C5 CRC64;

Query Match 79 %; Score 1861.5; DB 2; Length 428;

Best Local Similarity 86.0%; Pred. No. 9.5e-123;

Matches 363; Conservative 25; Mismatches 33; Indels 1; Gaps 1;

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 QY 361 GYLRDVSQNTYASPVVAGAFLLSGSGLLTLPHF- CFSFTTSGPDLVTEALDTKVP 419
 Db 361 GYLRDVSQNTYASPVVAGAFLLSGSGLLTLPHF- CFSFTTSGPDLVTEALDTKVP 420
 QY 420 KE 421
 Db 421 KE 422
 RESULT 6
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 AC Q8CF46;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 20.
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 DN clone:1700007D07 product:RIKEN cDNA 1700007D07.
 GN Name=Slc16a13;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RM Methods Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX Pubmed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritsch M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilmong L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Attalaya R.N., Bailey T.L., Banerai M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Cui M., Dalia E., Dalymphe B.P., de Bono B., Della Gatta G., di Bernardo C., Down T., Engstrom P., Fagioli S., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummelbeck L., Jacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kojima Y., Kishimoto S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mortrud T., Nabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlandi V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sanderlin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,

RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide A., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Atakawa T.,
 RA Iida J., Imanura K., Itoh M., Kato T., Kawai H., Kawagashira T.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nishimura N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.,
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX PubMed=16141073; DOI=10.1126/science.1112609;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RT (Genome Network Core Team) and the FANTOM Consortium;
 RL "Antisense transcription in the Mammalian Transcriptome.";
 RN Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22554683; PubMed=1246651; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
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 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs.";
 RN Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Aizawa K., Yoshino M., Itoh M., Ishii Y.,
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 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
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 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaeis P.,
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 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carlini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to
 RL prepare full-length cDNA libraries for rapid discovery of new genes.";
 RN Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki D., Carlini P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.";
 RN Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
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 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
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 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC
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 CC Distributed under the Creative Commons Attribution-NonCommercial License
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 CC EMBL: AK005699; BAC25120.1; -; mRNA.
 DR Ensembl: ENSMUSG00000044367; Mus musculus.
 DR MGI: MGI:1916559; Slc16a13.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0016020; C: membrane; IEA.
 DR GO: GO:0005215; F: transporter activity; IEA.
 DR GO: GO:0006810; P: transport; IEA.
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 DR Pfam: PF07690; MFS_1.
 DR PROSITE: PS00850; MFS_1.
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 QY 154 TPAFFOMILSHYARGLSLVSALSLHVAACGALLRPSLLEDPAYGPRPOLSLHH 213
 61 AFAPLFGOMLNNYARGALLVSALSILHMACGALLRPLSLTEDAAVGGFQAIITSLHH 120
 QY 214 GEPFLRYVALTLINIGYPIFYLAHVAHODLWDPLPAAFILSVVAISDVLGRVVGWLG 273

271 DRGLGCVGAALVVAAMADAGARLVCGMLADGQWVLPRLALVPAFLGLGLVTVGLVLP 330
 Y 300 VQAQPTA---LVALAVAYGFTSGALAPLAFSVLPPELIGTRRIYCGILQMIIESIGLL 355
 Y 331 VVGGESEWGGPFLAAVAAYVLSAGSYAPLVFGLPGLVGVGVQATGVMMLMSIGLL 390
 Y 356 GPPLSGYLARDVSGNYTASPVVAAFLISGSGILLTLPHFCSFTTSSGPODLVTEALDTK 415
 b 391 GPPLSGFLRDETDFTASFLISGSLILSSGFYIGLPR-----ALPSCGP-----ASPPA 440
 Y 416 VLPRKGLBGLNSTESGPESQS-LTARG 443
 b 441 TPPETG-----ELLPAQVALLSP 461
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 T 21-FEB-2006, entry version 8.
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 A Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
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 A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 A Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 A Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
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 A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 T "Generation and initial analysis of more than 15,000 full-length human
 T and mouse cDNA sequences.";
 L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 N [2]
 P NUCLEOTIDE SEQUENCE.
 C TISSUE=Ovary;
 C NIH MGC Project;
 L Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 C -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 C similarity).
 C Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 C Distributed under the Creative Commons Attribution-NonDerivative license
 C
 EMBL; BC098892; AAH98892.1; -, mRNA.
 ZFIN; ZDB-GENE-050706-122; zgc:114041.
 GO; GO:0016021; C:integral to membrane; IEA.
 GO; GO:0016020; C:membrane; IEA.
 GO; GO:0005215; F:transporter activity; IEA.
 GO; GO:0006810; P:transport; IEA.
 InterPro; IPR007114; MFS.
 Pfam; PF07690; MFS_1; 1.
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KM Hypothetical protein; Membrane; Transmembrane; Transport.
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 Y 6 EPPDGGWRVAVLAFPSQALVFGVLSFGVFVEFVAAFEQARVSWISIGIAVOQF 65
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 Y 186 GALLRP--PSLAEDPAV-----GSPRAQLT--SLHHGPELRITVALTLINTGYFIY 234
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 Y 295 LALFPVAQAPTALVAVAYGFTSGALAPLAFSVLPPELIGTRRIYCGILQMIIESIGL 354
 Db 307 LLLLEIAYGWSVAVFTSLXGFLFCGVAAIHVTSVVDLVGLEGFPASGLFMLNLSIGF 366
 Y 366 LCPPLSGYLARDVSGNYTASPVVAG-AFLISGSGILL-----TLPHFPCS 398
 Db 367 LCPPPAAGLVMDTTHNFCAFLISGICLLISGCFVVLVDMLVEKKKKKLOETL----- 419
 Y 399 TTSSGPODLVTEALDTK 415
 Db 420 -----QDPCTETTDLK 430
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 ID Q801R0_XENLA
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 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 21-FEB-2006, entry version 19.
 DE Slc16a6-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
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 C TISSUE=Embryo.
 X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 A Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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 A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,


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RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=1245917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RT Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RL initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.;  
CC Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By  
CC similarity).  
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DR EMBL; BC047967; AAH47967.1; -, mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR007114; MFS.  
DR InterPro; IPR011701; MFS_1.  
DR Pfam; PF07690; MFS_1; 1.  
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y 65 FGSVGSALSTKFCPRPVVMGTGLIALGMTLASPATSLLHLTLSTGLSSGMAITAP 124  
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b 81 FTABLSTLVSNRFCHRVVVMVGILISTGNITVASPSVEMVTVTIGLTSGYGCTFLP 140  
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y 125 TLVCLSTCYFERRRSLATGALTGVGLSSFTAPFFOMLSHYAMRGSLIVALSHTYA 184  
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b 141 TVTTLSOYFEKRSLTYAAVASTGECAFAFAFADPALNALNNLKMYCLTIYGAQLNIV 200  
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y 185 CGALLR----PELSAEDPA----- 199  
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c 201 CGSLIRPIVIKPDEVKSPAKPENLETMTLENEDTLTSVDSDSGVEVSTPKXNVASM 260  
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c 200 -----VGPPRAOLT-----SLHHGFPLRYTVALTLINGYIIFPLHL 237  
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b 321 PLISLSIGINKOLSAVYMKSNAHAISVFPRISAGMITLNKKPMRKRIYLIVFWLLCVALLA 380  
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TOPO DOM 408 492 Cytoplasmic (Potential).
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Best Local Similarity 36.1%; Pred. No. 5e-37;
Matches 170; Conservative 70; Mismatches 193; Indels 38; Gaps 9;

3 RRRPPGCGGRVVVLSAFPGSALVFCVLRSEFGVPEVFAVFAEQARVMSISGLAV 62
8 RGACPPDGGWGVVAGACFVITGFAVFPKAVSVFFRELKDFAGAGSDTAWVSIMLAM 67
63 QOFSPVGSALSTKCPRPVMTGILALGMLASFATSLTHLYISIGLSSGMAITF 122
68 LYGTGPLSSILVTRFCGRPVMLAGGLASAGMILASFASRLLELYTAGVLTGLALNF 127
123 APTLACISCYRRSLATGALTGVGSSFTFAPFQWMLSHYAMGSLLVASLHL 182
128 QPSLIMGLYERRRPLANGLAAGSPVFLSTLSPLGQLGERGMRGFLFGGLLHC 187
183 VACGALLRPPELAE--DPAVGGPRAQLTSLH-----HGPFLEYALTLLINTGFIPY 234
188 CACGAVRRPQCPQPRDPAPGGRARHQLDLAVCDRTFMVYWKPLMALGLFVPA 247
235 LHLVAHLDLMDPLPAAFLLISVAISDLVGRVVG--WLGDVPGVTRTLMMLTTLT 291
248 ILLVYAKADAVPDAEAFLLSIVGFVIVARPCAGLAGLRLP-HVPLFSLITALIAN 306
292 GVSLLAFVPAAPFALVLAAYGFTSGALPLAFSVLPGLIGTRIRYCGILQMTESI 351
307 GLTDLISARASVGTLLVAFCTAFGLSYGMVALQEVIMATVAVRPSALGLVLVEAV 366
352 GGLGPPPLSGYLRDVSGNYTASFVAVAGFLSSGILLTLPHFCFSTT----- 400
367 AVLLGPPSAGLVDAIKNYEIIIFYLAGS-EVALACVFNAAVTTYCCLRCKSISSGRSAG 425
401 -TSGPQDLVTEALDTKVPDPKEGLEGLNSTEGESQSLTAPGILLPRLG 450
426 GASDPEDV--EAERDSEMPA-----STE--EPGLEALEVLSPRAG 463

RESULT 13
JUCO_MOUSE PRELIMINARY; PRT; 290 AA.
09JUCO_MOUSE
01-OCT-2000, integrated into UniProtKB/TrEMBL.
01-OCT-2000, sequence version 1.
07-FEB-2006, entry version 21.
Mus musculus brain cDNA, clone MNCB-2717 (Novel RNA polymerase Rpb1 C-terminal repeat domain containing protein).
Name=Slc16a1; Synonyms=RP23-198E14.4; ORFNames=RP23-198E14.4-003;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridea; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL.
Oseida N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
Hashimoto K.,
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[2]
NUCLEOTIDE SEQUENCE.
Sycamore N.,
Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AB041591; BAA95074.1; -; mRNA.
DR EMBL; AL669869; CA135221.1; -; Genomic DNA.
DR EMBL; ENSMUSG0000040938; Mus musculus.
DR MGI; MGI:2663709; Slc16a1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 290 AA; 29031 MW; AA5501FCA7ED7P9F CRC64;

Query Match 27.6%; Score 643; DB 2; Length 290;
Best Local Similarity 47.4%; Pred. No. 3.9e-37;
Matches 138; Conservative 43; Mismatches 94; Indels 16; Gaps 4;

QY 84 MNGGILALGMLASFATSLTHLYISIGLSSGMAITFAPPTACSCYFSRRSLATGL 143
1 MNGGVLTSLGVLFSARSLHLYLGLGLAGSGMALVFAPALGTSRYSRRRVLAAGL 60
QY 144 ALTGVLSSFTFAPFQWMLSHYAMRGSLLVSAISLHVACGALLRPSLADPAVGP 203
61 ALTGNGASSILLAPALQPLDFTGMRGALLLGAIVTLHTPCGALLRPLASDDP-LAP 119
DB 204 RAQLTS---LHNGPFLRYVALTLINTGFIPYHLYVAHLDLMDPLPAFLLSYVA 259
120 RTPLALGLGLFRRRAFSVAFALGTALIGGYFVYVHLGPHALDQMGYGAALVAVAA 179
QY 260 ISDLVGRVSGMDGDAVPGVTRTLMMLTTLNGVSLALFPVAQPTA-----LV 310
180 VGDACARLASGWLADGQWPLPRLVAVFGSLTG--LGVLMGIVPTVGTGEGCAPILAA 237
QY 311 AVAVGFTSGALPLAFSVLPGLIGTRIRYCGILQMTESIGLGPPLSG 361
238 AGAVGLSAGSVAPLVGVLPGLVIGGVQATGSLVMMMSIGLGLPPLSG 288
DB

RESULT 14
08BGC3_MOUSE PRELIMINARY; PRT; 486 AA.
ID 08BGC3_MOUSE
AC 08BGC3_MOUSE
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE 14, 17 days embryo head cDNA, RIKEN full-length enriched library,
clone:3230401A21 product:hypothetical protein, full insert sequence
DE (10 days neonate skin cDNA, RIKEN full-length enriched library,
clone:4732488P05 product:hypothetical protein, full insert sequence).
GN Name=Slc16a12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head and Skin.
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6679(99)03004-9;
RA Carinci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batilov S., Forrest A.R., Zavolan M.,
[2]
NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Head and Skin.
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carinci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batilov S., Forrest A.R., Zavolan M.,

RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Banerai M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingras T., Grigoriou T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Ueki N., Kanapin A., Katoh M., Kawasawa Y., Kelso A., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Laveau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liumi S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Motestegui-Tobar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shihata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,
RA Tammola K., Tan S.L., Tang S., Taylor M.S., Tegner J., Telchmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamashita H., Zaborovskiy E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Mahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RA "The transcriptional landscape of the mammalian genome.",
RA Science 309:1559-1563(2005).
[3]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RA (Genome Network Core Team) and the FANTOM Consortium;
RA "Antisense Transcription in the Mammalian Transcriptome.",
RA Science 309:1564-1566(2005).
[4]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chotila C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nomura K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Wilming L.G., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
RA Hironaka-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.",
RA Nature 420:563-573(2002).
[5]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA MEDLINE=1085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriquez I., Sakamoto N.,
RA Norone P., Ring B., Ringwald M., Rodriquez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Watanabe Y., Yoshida K., Hasegawa Y., Kawai J., Kohlschki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.",
RA Nature 409:665-690(2001).
[6]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RA prepare full-length cDNA libraries for rapid discovery of new genes.",
RA Genome Res. 10:1617-1630(2000).
[7]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashwagi K.,
RA Fujimori S., Inoue K., Togawa K., Ozawa K., Tanaka T., Matsura S.,
RA Yoneda Y., Ishikawa T., Otsu N., Iwama M., Ohara E., Watanabe M.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RA sequencing pipeline with 384 multiplexed sequencer.",
RA Genome Res. 10:1757-1771(2000).
[8]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hoti F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Tanaka Y., Tanaka T.,
RA Tomaru Y., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (Jul-2001) to the EMBL/GenBank/DBD databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC EMBL, AK02076; BAC26279.1; -, mRNA.
CC EMBL, AK028284; BAC25857.1; -, mRNA.
CC Ensembl; ENSMUSG00000009378; Mus musculus.

MGI: 2147716; Slc16a12.
GO: GO:0016021; C: integral to membrane; IEA.
GO: GO:0016020; C: membrane; IEA.
GO: GO:0005215; F: transporter activity; IEA.
GO: GO:0006810; P: transport; IEA.
InterPro: IPR007114; MFS.
InterPro: IPR011701; MFS_1.
Pfam: PF07690; MFS_1.
PROSITE: PS50850; MFS; 1.
Hypothetical protein: Membrane, Transmembrane, Transport.
SEQUENCE 486 AA; 53152 MW; AA3CC951FB28247 CRC64;

Query Match 27.5%; Score 640; DB 2; Length 486;
Best Local Similarity 32.1%; Pred. No. 1.1e-36;
Matches 152; Conservative 89; Mismatches 172; Indels 60; Gaps 7;

7 PPDGGMGRVVVLSAFQSAVFGVLRSPGVFVEFVAAFEQAAVSVIASIGIAVQOFG 66
12 PPDGGMGRVVVLSAFQSAVFGVLRSPGVFVEFVAAFEQAAVSVIASIGIAVQOFG 71
67 SPVGSALSTKCPRPVMTGGLAALGMLASFATSLTHLYISIGLSSGVALTEAPTL 126
72 APLGSVNSNOLSCQAGIMLGLASTGFLIGSFATSLKHLVLSLGLGALCYSPAI 131
127 ACLSCYFSRRSLATGALTGVLSFTFAPFQWMLSHYAWRGSLVLSALSLHVAAG 186
132 AMVKYFSRRKALAVGIAMSGSIGITFILAPVQULIEQFSWKGALLIGFVNLGCVG 191
187 ALRPPSLAEDPAV-----GGPRAQLT-----SLHHPPLRYT 220
192 ALMRITTLKEDSVPEKHNRESQEDCKQASPSPLTKECTETRLCSLQOEYGLIMS 251
221 VALTLINCYIFPY-----LHLVAHLODLDPLPAAFLLSVASISDYGVSGLMD 274
252 DFVVAASVLFMAVYGCSPFLVYLVPAALSVGVSHOQAFMLSLIGVITDVGNTGMLTD 311
275 AVPGVTRLL-----MLMTTLTGVSLALFPVAQAPTAVALAVAYGFTSGALAPLAF 326
312 -----RRLKNYQVYCYLFAVALDGLCYLCLPMQLTFPLVDFSCTFGYPDGAAYVTLLP 365
327 SVLPFLIGTRIRYICGLIOMIESIGLGLPPLSGYLRVSGNYTASFYVAQAFLLSGG 386
366 VVTAEIVGTSSLSALGVYFLHVAPLYVSPPIAGLVDTGSYTAAPFLCG-FAAIFSS 424
387 LLTLTLPHFCTTTSGPDVLTVALDTPVLPKKEGLEGLNSTESGSPQSQT 439
425 ILL-----GVYRIVAKMKRTQVFPFVKSDPKQLQMTNGSVAYSV 464

SUPL 15
F732 HUMAN
O5TJ32_HUMAN PRELIMINARY; PRT; 463 AA.
O5TJ32; 21-DEC-2004, integrated into UniProtKB/TrEMBL.
21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 11.
Soluble carrier family 16 (Monocarboxylic acid transporters), member 12 (Fragment)
ORFNames: RPI1-169010.10-001;
Homo sapiens (Human).
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
Homo.
NCBI_TaxID=9606;
[1]
NUCLEOTIDE SEQUENCE.
Chapman J.
Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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EMBL: AL353146; CA112383.1; -; Genomic_DNA.

DR Ensembl; ENSG00000152779; Homo sapiens.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005215; F: transporter activity; IEA.
DR GO: GO:0006810; P: transport; IEA.
InterPro: IPR007114; MFS.
InterPro: IPR011701; MFS_1.
Pfam: PF07690; MFS_1.
PROSITE: PS50850; MFS; 1.
DR NON TER 463
FT 463
SEQUENCE 463 AA; 50570 MW; C38CA95E85D338DF CRC64;

Query Match 27.3%; Score 637.5; DB 2; Length 463;
Best Local Similarity 33.5%; Pred. No. 1.6e-36;
Matches 146; Conservative 83; Mismatches 144; Indels 63; Gaps 9;

2 ARTEPPDGMGRVVVLSAFQSAVFGVLRSPGVFVEFVAAFEQAAVSVIASIGIA 61
37 ARSTSPDGMGRVVVLSAFQSAVFGVLRSPGVFVEFVAAFEQAAVSVIASIGIA 96
62 VQFGSPVGSALSTKCPRPVMTGGLAALGMLASFATSLTHLYISIGLSSGVALT 121
97 VTMLCAPLGSVNSNOLSCQAGIMLGLASTGFLIGSFATSLKHLVLSLGLGALCY 156
122 FAPTLACLSCYFSRRSLATGALTGVLSFTFAPFQWMLSHYAWRGSLVLSALSLH 181
157 YSPAIAMVKYFSRRKALAVGIAMSGSIGITFILAPVQULIEQFSWKGALLIGFV 216
182 LVACGALLRPPSLAEDPAV-----GGPRAQLT-----SLHHPPLRYT 220
217 LCVGALLMRPITTLKEDSVPEKHNRESQEDCKQASPSPLTKECTETRLCSLQOE 276
210 LHHGPFRLRYVALTLINTG-----YFIRY-LHL-VAHLODLDPLPAAFLLSV 261
277 FLMSDFVLAASVLFMAVYGCSPFLVYLVPAALSVGVSHOQ-----AAFLMS 328
262 DLVGRVSGWGDVAPGVTLL-----MLMTTLTGVSLALFPVAQAPTAVALAVA 313
329 DIGNITFGMLTD-----RRLKNYQVYCYLFAVALDGLCYLCLPMQLTFPLV 362
314 YGFTSGALAPLAFSVLPFLIGTRIRYICGLIOMIESIGLGLPPLSGYLRVSGNY 373
383 FGYPDGAAYVTLLIPVTTIEIVGTSSLSALGVYFLHVAPLYVSPPIAGLVDTG 442
374 FYVAQAFLLSGSGILL 389
443 FLICG-FSMIFSSVLL 457

Search completed: September 7, 2006, 13:07:17
Job time : 305 secs

b 301 AOAFTALVALAAYGFTSGALAPLAFSVLPBELIGTRRIYCGLLQMIRESIGLLGPPLS 360
y 361 GYLKRVDSGNVTASFFVAGAFLLSGSGLLTLPHFECFSTTTSGPQDLVTEALDTKVPLEK 420
b 361 GYLKRVDSGNVTASFFVAGAFLLSGSGLLTLPHFECFSTTTSGPQDLVTEALDTKVPLEK 420
y 421 EGLEGLNSTESGESQSILTAPGLLPRIGLHRTVP 457
b 421 EGLEGLNSTESGESQSILTAPGLLPRIGLHRTVP 457
RESULT 2
S-10-654-428-2
Sequence 2, Application US/10654428
Publication No. US20040082035A1
GENERAL INFORMATION:
APPLICANT: KERCHUK, Karen et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001013CIP-CON
CURRENT APPLICATION NUMBER: US/10/654,428
CURRENT FILING DATE: 2003-09-04
PRIOR APPLICATION NUMBER: 09/829,432
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 09/815,301
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/254,554
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 457
TYPE: PRT
ORGANISM: Homo sapiens
S-10-654-428-2
Query Match 100.0%; Score 2331; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.8e-194;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 1 MARRTEPPDGGMGRRVYVLSAFQSAIVFGVLRSGFVEFVAAFEBOAARVSWIASIGI 60
b 1 MARRTEPPDGGMGRRVYVLSAFQSAIVFGVLRSGFVEFVAAFEBOAARVSWIASIGI 60
y 61 AVQOFGSPVGSALSTKFGPRPVMTGGILALGMLASFATSLTHLYLSIGLLSGGMA 120
b 61 AVQOFGSPVGSALSTKFGPRPVMTGGILALGMLASFATSLTHLYLSIGLLSGGMA 120
y 121 TPAPTACLSYCFRRRSRLATGALTGVGLSFTFPAFFQWMLSHYAMRGSLLVSALS 180
b 121 TPAPTACLSYCFRRRSRLATGALTGVGLSFTFPAFFQWMLSHYAMRGSLLVSALS 180
y 181 HLVAAGCALLRPPSLADPAVGGPRAQLTSLHHGPFLRYTVALTTLINTGYFIPYLHVAH 240
b 181 HLVAAGCALLRPPSLADPAVGGPRAQLTSLHHGPFLRYTVALTTLINTGYFIPYLHVAH 240
y 241 LQDLMDPPLPAFFLSVVAISDLVGRVVGMDGDAVGPVTRLMLMTTLTGVSIALFPV 300
b 241 LQDLMDPPLPAFFLSVVAISDLVGRVVGMDGDAVGPVTRLMLMTTLTGVSIALFPV 300
y 301 AOAFTALVALAAYGFTSGALAPLAFSVLPBELIGTRRIYCGLLQMIRESIGLLGPPLS 360
b 301 AOAFTALVALAAYGFTSGALAPLAFSVLPBELIGTRRIYCGLLQMIRESIGLLGPPLS 360
y 361 GYLKRVDSGNVTASFFVAGAFLLSGSGLLTLPHFECFSTTTSGPQDLVTEALDTKVPLEK 420
b 361 GYLKRVDSGNVTASFFVAGAFLLSGSGLLTLPHFECFSTTTSGPQDLVTEALDTKVPLEK 420
y 421 EGLEGLNSTESGESQSILTAPGLLPRIGLHRTVP 457
b 421 EGLEGLNSTESGESQSILTAPGLLPRIGLHRTVP 457

RESULT 3
US-10-451-168-110
; Sequence 110, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-451-168-110
Query Match 92.4%; Score 2154; DB 4; Length 426;
Best Local Similarity 99.8%; Pred. No. 8.9e-179;
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
y 1 MARRTEPPDGGMGRRVYVLSAFQSAIVFGVLRSGFVEFVAAFEBOAARVSWIASIGI 60
b 1 MARRTEPPDGGMGRRVYVLSAFQSAIVFGVLRSGFVEFVAAFEBOAARVSWIASIGI 60
y 61 AVQOFGSPVGSALSTKFGPRPVMTGGILALGMLASFATSLTHLYLSIGLLSGGMA 120
b 61 AVQOFGSPVGSALSTKFGPRPVMTGGILALGMLASFATSLTHLYLSIGLLSGGMA 120
y 121 TPAPTACLSYCFRRRSRLATGALTGVGLSFTFPAFFQWMLSHYAMRGSLLVSALS 180
b 121 TPAPTACLSYCFRRRSRLATGALTGVGLSFTFPAFFQWMLSHYAMRGSLLVSALS 180
y 181 HLVAAGCALLRPPSLADPAVGGPRAQLTSLHHGPFLRYTVALTTLINTGYFIPYLHVAH 240
b 181 HLVAAGCALLRPPSLADPAVGGPRAQLTSLHHGPFLRYTVALTTLINTGYFIPYLHVAH 240
y 241 LQDLMDPPLPAFFLSVVAISDLVGRVVGMDGDAVGPVTRLMLMTTLTGVSIALFPV 300
b 241 LQDLMDPPLPAFFLSVVAISDLVGRVVGMDGDAVGPVTRLMLMTTLTGVSIALFPV 300
y 301 AOAFTALVALAAYGFTSGALAPLAFSVLPBELIGTRRIYCGLLQMIRESIGLLGPPLS 360
b 301 AOAFTALVALAAYGFTSGALAPLAFSVLPBELIGTRRIYCGLLQMIRESIGLLGPPLS 360
y 361 GYLKRVDSGNVTASFFVAGAFLLSGSGLLTLPHFECFSTTTSGPQDLVTEALDTKVPLEK 420
b 361 GYLKRVDSGNVTASFFVAGAFLLSGSGLLTLPHFECFSTTTSGPQDLVTEALDTKVPLEK 420
y 421 EGLE 424
b 421 EGLE 424

Db 421 EGLE 424

RESULT 4
US-10-980-387-110

/ Sequence 110, Application US/10980387
/ Publication No. US20050164343A1
/ GENERAL INFORMATION:
/ APPLICANT: SMITHKLINE BEECHAM CORPORATION
/ APPLICANT: SMITHKLINE BEECHAM P.L.C.
/ APPLICANT: GLAXO GROUP LIMITED
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50039
/ CURRENT APPLICATION NUMBER: US/10/980,387
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US/10/980,387
/ PRIOR FILING DATE: 2003-11-0312
/ PRIOR APPLICATION NUMBER: PCT/US01/49232
/ PRIOR FILING DATE: 2000-12-17
/ PRIOR APPLICATION NUMBER: 60/256,710
/ PRIOR FILING DATE: 2000-12-19
/ PRIOR APPLICATION NUMBER: 60/257,048
/ PRIOR FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 60/260,482
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: 60/264,922
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/266,797
/ PRIOR FILING DATE: 2001-02-06
/ PRIOR APPLICATION NUMBER: 60/276,988
/ PRIOR FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 60/281,535
/ PRIOR FILING DATE: 2001-04-04
/ PRIOR APPLICATION NUMBER: 60/289,622
/ PRIOR FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 110
/ LENGTH: 426
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ JS-10-980-387-110

Query Match 92.4%; Score 2154; DB 5; Length 426;
Best Local Similarity 99.8%; Pred. No. 8,9e-119;
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MARRTEPPDGMGKVVVLSAFQSGALVGVLSFGVFEVEFVAAFEBQAAVSWIASIGI 60
b 1 MARRTEPPDGMGKVVVLSAFQSGALVGVLSFGVFEVEFVAAFEBQAAVSWIASIGI 60
Y 61 AVOQFGSPVGSALSTKRGPRVVMVTGGILAAAGMLASFATSLTHLYSLIGLSSGSMAL 120
b 61 AVOQFGSPVGSALSTKRGPRVVMVTGGILAAAGMLASFATSLTHLYSLIGLSSGSMAL 120
Y 121 TFAPTLACLSGCVSRRSLATGALTGVGLSPTFAFPOMLSHYAMRGSLLVSLSL 180
b 121 TFAPTLACLSGCVSRRSLATGALTGVGLSPTFAFPOMLSHYAMRGSLLVSLSL 180
Y 181 HAVACGALRPPSLAEDPAVGGPRAOLTSLLHGPFLRYVAALTLNTGFTFYHLVAH 240
b 181 HAVACGALRPPSLAEDPAVGGPRAOLTSLLHGPFLRYVAALTLNTGFTFYHLVAH 240
Y 241 LQDLDDPPLPAFLISVVAISDLVGRVSGMLGDAVGPVTRLLMLMTLLTGVSALFPV 300
b 241 LQDLDDPPLPAFLISVVAISDLVGRVSGMLGDAVGPVTRLLMLMTLLTGVSALFPV 300
Y 301 AOPATLVAALVAVYGTSGALAPLAFSVLPBLIGTRIRYCGIGLLQMISSIGLGPPLS 360
b 301 AOPATLVAALVAVYGTSGALAPLAFSVLPBLIGTRIRYCGIGLLQMISSIGLGPPLS 360
Y 361 GYLRDVSGNVTASFVAVAGFLSSGIGILLTPHFPCFSTTSGPODVTALDTKVPJPK 420
b 361 GYLRDVSGNVTASFVAVAGFLSSGIGILLTPHFPCFSTTSGPODVTALDTKVPJPK 420

Db 361 GYLRDVSGNVTASFVAVAGFLSSGIGILLTPHFPCFSTTSGPODVTALDTKVPJPK 420
Qy 421 EGLE 424
Db 421 EGLE 424

RESULT 5

US-10-297-022-16
/ Sequence 16, Application US/10297022
/ Publication No. US20030216310A1
/ GENERAL INFORMATION:

/ APPLICANT: INCYTE GENOMICS, INC.
/ APPLICANT: THORNTON, Michael
/ APPLICANT: WALIA, Nandinder K.
/ APPLICANT: YUE, Henry
/ APPLICANT: NGUYEN, Daniel B.
/ APPLICANT: LAL, Preeti
/ APPLICANT: GANDHI, Ameena R.
/ APPLICANT: TRIBOULEY, Catherine M.
/ APPLICANT: YAO, Monique G.
/ APPLICANT: RAMKUMAR, Jayalaxmi
/ APPLICANT: AU-YOUNG, Janice
/ APPLICANT: LU, Yan
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: AZIMZAI, Yalda
/ APPLICANT: BRUNS, Christopher M.
/ APPLICANT: GRIFFIN, Jennifer A.
/ APPLICANT: YANG, Junming
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: SANJANWALA, Madhu S.
/ APPLICANT: RAUMANN, Brigitte E.
/ APPLICANT: LEE, Ernestine A.
/ APPLICANT: HAFALIA, April
/ APPLICANT: GREENE, Barrie D.
/ APPLICANT: KHAN, Farrah A.
/ APPLICANT: KEARNEY, Liam
/ APPLICANT: ELLIOTT, Vicky S.
/ APPLICANT: SEILHAMER, Jeffrey J.
/ APPLICANT: POLICKY, Jennifer L.
/ APPLICANT: BOROWSKY, Mark L.
/ APPLICANT: BURFORD, Neil
/ APPLICANT: DING, Li
/ APPLICANT: LU, Dying Aina M.
/ APPLICANT: HILLMAN, Jennifer L.
/ TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
/ FILE REFERENCE: PI-0109 PCT
/ CURRENT APPLICATION NUMBER: US/10/297,022
/ PRIOR FILING DATE: 2002-11-25
/ PRIOR APPLICATION NUMBER: 60/208,424; 60/209,001; 60/210,588; 60/212,335; 60/213,747;
/ PRIOR FILING DATE: 2000-05-26; 2000-06-01; 2000-06-08; 2000-06-16; 2000-06-22; 2000-06-26
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PERL Program
/ SEQ ID NO 16
/ LENGTH: 426
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20030216310A1 817477CD1
US-10-297-022-16

Query Match 92.3%; Score 2151; DB 4; Length 426;
Best Local Similarity 99.5%; Pred. No. 1,6e-178;
Matches 422; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARRTEPPDGMGKVVVLSAFQSGALVGVLSFGVFEVEFVAAFEBQAAVSWIASIGI 60
Db 1 MARRTEPPDGMGKVVVLSAFQSGALVGVLSFGVFEVEFVAAFEBQAAVSWIASIGI 60
Qy 61 AVOQFGSPVGSALSTKRGPRVVMVTGGILAAAGMLASFATSLTHLYSLIGLSSGSMAL 120
Db 61 AVOQFGSPVGSALSTKRGPRVVMVTGGILAAAGMLASFATSLTHLYSLIGLSSGSMAL 120

Y 121 TFAPTLACLSCEFSRRRSIATGIALTGVLSSFTFAPFFOMLISHYAMRGSLIVSALS 180
Y 121 TFAPTLACLSCEFSRRRSIATGIALTGVLSSFTFAPFFOMLISHYAMRGSLIVSALS 180
b 121 TFAPTLACLSCEFSRRRSIATGIALTGVLSSFTFAPFFOMLISHYAMRGSLIVSALS 180
Y 181 HUVACGALLRPPSLAEDPAVGGPRAQLTSLIHGPFRLRYTVALTLINTGYFIPYHLVAH 240
b 181 HUVACGALLRPPSLAEDPAVGGPRAQLTSLIHGPFRLRYTVALTLINTGYFIPYHLVAH 240
Y 241 LODLMDPPLPAAFLLSVVAISDLVGRVSGMLGDAVPGPVTRLMLMTTLTGVSALFPV 300
b 241 LODLMDPPLPAAFLLSVVAISDLVGRVSGMLGDAVPGPVTRLMLMTTLTGVSALFPV 300
Y 301 AQAFTALVALAVYGFSGALAPLAFSVLPBLIGTRRIYCGILQIMIESIGLGPPLS 360
b 301 AQAFTALVALAVYGFSGALAPLAFSVLPBLIGTRRIYCGILQIMIESIGLGPPLS 360
Y 361 GYLKRVSGNVTASFVAGAFLLSGGILLTLPHFPCFSTTSGPDLVTEALDTKVPK 420
b 361 GYLKRVSGNVTASFVAGAFLLSGGILLTLPHFPCFSTTSGPDLVTEALDTKVPK 420
Y 421 EGLE 424
b 421 EGLE 424

RESULT 6
S-10-072-012-306
Sequence 306, Application US/10072012
Publication No. US2004003493A1
GENERAL INFORMATION:
APPLICANT: Tchervnev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernhusen, Bryan
APPLICANT: Patnureajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie E.
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grose, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072.012
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057

;; PRIOR FILING DATE: 2001-02-07
;; PRIOR APPLICATION NUMBER: 60/266,975
;; PRIOR FILING DATE: 2001-02-07
;; PRIOR APPLICATION NUMBER: 60/267,459
;; PRIOR FILING DATE: 2001-02-08
;; Remaining Prior Application data removed - See file wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1391
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 306
;; LENGTH: 426
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-072-012-306

Query Match 92.2%; Score 2150; DB 4; Length 426;
Best Local Similarity 99.5%; Pred. No. 2e-178;
Matches 422; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARTEPPDGGKGRVULSAFFQSALVFGVLRSGVCFVEFVAFAEEOARVSWIASIGI 60
DB 1 MARTEPPDGGKGVVLSAFFQSALVFGVLRSGVCFVEFVAFAEEOARVSWIASIGI 60
QY 61 AVQDFGSPVGSALSTKFGPRPVMTGIIAAGMLASFATSLTLHYISIGLSSGNAL 120
DB 61 AVQDFGSPVGSALSTKFGPRPVMTGIIAAGMLASFATSLTLHYISIGLSSGNAL 120
QY 121 TFAPTLACLSCEFSRRRSIATGIALTGVLSSFTFAPFFOMLISHYAMRGSLIVSALS 180
DB 121 TFAPTLACLSCEFSRRRSIATGIALTGVLSSFTFAPFFOMLISHYAMRGSLIVSALS 180
QY 181 HUVACGALLRPPSLAEDPAVGGPRAQLTSLIHGPFRLRYTVALTLINTGYFIPYHLVAH 240
DB 181 HUVACGALLRPPSLAEDPAVGGPRAQLTSLIHGPFRLRYTVALTLINTGYFIPYHLVAH 240
QY 241 LODLMDPPLPAAFLLSVVAISDLVGRVSGMLGDAVPGPVTRLMLMTTLTGVSALFPV 300
DB 241 LODLMDPPLPAAFLLSVVAISDLVGRVSGMLGDAVPGPVTRLMLMTTLTGVSALFPV 300
QY 301 AQAFTALVALAVYGFSGALAPLAFSVLPBLIGTRRIYCGILQIMIESIGLGPPLS 360
DB 301 AQAFTALVALAVYGFSGALAPLAFSVLPBLIGTRRIYCGILQIMIESIGLGPPLS 360
QY 361 GYLKRVSGNVTASFVAGAFLLSGGILLTLPHFPCFSTTSGPDLVTEALDTKVPK 420
DB 361 GYLKRVSGNVTASFVAGAFLLSGGILLTLPHFPCFSTTSGPDLVTEALDTKVPK 420
QY 421 EGLE 424
DB 421 EGLE 424

RESULT 7
US-10-072-012-338
Sequence 338, Application US/10072012
Publication No. US2004003493A1
GENERAL INFORMATION:
APPLICANT: Tchervnev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernhusen, Bryan
APPLICANT: Patnureajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie E.
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A

APPLICANT: Furtak, Katarzyna
 APPLICANT: Grosse, William M.
 APPLICANT: Alsobrook II, John P.
 APPLICANT: Lepley, Denise M.
 APPLICANT: Rieger, Daniel K.
 APPLICANT: Burgess, Catherine E.
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 21402-258
 CURRENT APPLICATION NUMBER: US/10/072,012
 PRIOR FILING DATE: 2002-01-31
 PRIOR APPLICATION NUMBER: 60/265,102
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: 60/265,514
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,517
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,412
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,395
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/266,406
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 60/266,767
 PRIOR FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: 60/267,057
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/266,975
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/267,459
 PRIOR FILING DATE: 2001-02-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1391
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 338
 LENGTH: 427
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (15)
 OTHER INFORMATION: wherein Xaa is any amino acid.
 S-10-072-012-338
 Query Match
 Best Local Similarity 91.9%; Score 2142.5; DB 4; Length 427;
 Matches 422; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Db 361 SCYLRDVNGNTASFWAGAFLLSGGILLTLPHFCESTTSGPDVTEALDKVPLP 420
 QY 420 KEGLE 424
 Db 421 KEGLE 425
 RESULT 8
 US-10-072-012-779
 ; Sequence 779, Application US/10072012
 ; Publication No. US2004003493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tcherev, Velizar
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Zetthuesen, Bryan
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Li, Li
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Taupier Jr, Raymond J.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Colman, Steven D.
 ; APPLICANT: Wclenc, Adam R.
 ; APPLICANT: Pena, Carol E. A
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Alsobrook II, John P.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Burgess, Catherine E.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-258
 ; CURRENT APPLICATION NUMBER: US/10/072,012
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,102
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 60/265,514
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,517
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,412
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,395
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/266,406
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/266,767
 ; PRIOR FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: 60/267,057
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: 60/266,975
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: 60/267,459
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1391
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 779
 ; LENGTH: 427
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (15)
 ; OTHER INFORMATION: wherein Xaa is any amino acid.
 US-10-072-012-779
 Query Match 91.9%; Score 2142.5; DB 4; Length 427;

Best Local Similarity 99.3%; Pred. No. 9e-178;
Matches 422; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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1 MARRTEPPDGGWG-RVVVLSAFQSAFYGVRSFGVFVEVVAFAFEQAAVSMIASIG 59
1 MARRTEPPDGGWG-RVVVLSAFQSAFYGVRSFGVFVEVVAFAFEQAAVSMIASIG 60
1 MARRTEPPDGGWG-RVVVLSAFQSAFYGVRSFGVFVEVVAFAFEQAAVSMIASIG 61
1 IAVQFGSPVGSALSTKFCPRPVMTGGILALGMLASFATSLTHLYISIGLSGSGMA 119
1 IAVQFGSPVGSALSTKFCPRPVMTGGILALGMLASFATSLTHLYISIGLSGSGMA 120
120 LTFAPTLACLSYCFRRRSRLATGALTGVGLSSFTFAPFPQMLSHYAMRGSLLVSALS 179
121 LTFAPTLACLSYCFRRRSRLATGALTGVGLSSFTFAPFPQMLSHYAMRGSLLVSALS 180
180 LHLVACGALLRPPSLAEDPAVGGPRAQLTSLHHGPFRLRYTALTINTGYFIPYHLVA 239
181 LHLVACGALLRPPSLAEDPAVGGPRAQLTSLHHGPFRLRYTALTINTGYFIPYHLVA 240
240 HLQDDMDPLPAFLLSVAISDLVGRVVSGLGDAVPGPVTRLMLMTTLTGVSIALFP 299
241 HLQDDMDPLPAFLLSVAISDLVGRVVSGLGDAVPGPVTRLMLMTTLTGVSIALFP 300
300 VAOAPTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLIGPPL 359
301 VAOAPTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLIGPPL 360
360 SGYLRVSGNTYASFVAGAFLLSGGILLTLPHFCSFTTSSGPODVTALDTRKVPPL 419
361 SGYLRVSGNTYASFVAGAFLLSGGILLTLPHFCSFTTSSGPODVTALDTRKVPPL 420
Y 420 EGLE 424
421 EGLE 425
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RESULT 9
S-10-072-012-302
Sequence 302, Application US/10072012
Publication No. US2004003493A1
GENERAL INFORMATION:
APPLICANT: Tchenerov, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernhusen, Bryan
APPLICANT: Patcurajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigatu, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517

PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 302
LENGTH: 426
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-302

Query Match 91.9%; Score 2142; DB 4; Length 426;
Best Local Similarity 99.1%; Pred. No. 9.9e-178;
Matches 420; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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1 MARRTEPPDGGWG-RVVVLSAFQSAFYGVRSFGVFVEVVAFAFEQAAVSMIASIG 60
1 MARRTEPPDGGWG-RVVVLSAFQSAFYGVRSFGVFVEVVAFAFEQAAVSMIASIG 61
1 IAVQFGSPVGSALSTKFCPRPVMTGGILALGMLASFATSLTHLYISIGLSGSGMA 120
1 IAVQFGSPVGSALSTKFCPRPVMTGGILALGMLASFATSLTHLYISIGLSGSGMA 121
121 TFAPTLACLSYCFRRRSRLATGALTGVGLSSFTFAPFPQMLSHYAMRGSLLVSALS 180
121 TFAPTLACLSYCFRRRSRLATGALTGVGLSSFTFAPFPQMLSHYAMRGSLLVSALS 181
181 HLVACGALLRPPSLAEDPAVGGPRAQLTSLHHGPFRLRYTALTINTGYFIPYHLVAH 240
181 HLVACGALLRPPSLAEDPAVGGPRAQLTSLHHGPFRLRYTALTINTGYFIPYHLVAH 241
241 LQDDMDPLPAFLLSVAISDLVGRVVSGLGDAVPGPVTRLMLMTTLTGVSIALFPV 300
241 LQDDMDPLPAFLLSVAISDLVGRVVSGLGDAVPGPVTRLMLMTTLTGVSIALFPV 301
301 AOPTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLIGPPLS 360
301 AOPTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLIGPPLS 361
361 GYLRVSGNTYASFVAGAFLLSGGILLTLPHFCSFTTSSGPODVTALDTRKVPPLK 420
361 GYLRVSGNTYASFVAGAFLLSGGILLTLPHFCSFTTSSGPODVTALDTRKVPPLK 421
421 EGLE 424
421 EGLE 425
DB 421 EGLE 424
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RESULT 10
US-10-072-012-304
Sequence 304, Application US/10072012
Publication No. US2004003493A1
GENERAL INFORMATION:
APPLICANT: Tchenerov, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernhusen, Bryan
APPLICANT: Patcurajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha

```

/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 304
/ LENGTH: 426
/ TYPE: PRT
/ ORGANISM: Homo sapiens
IS-10-072-012-304
Query Match          91.9%; Score 2142; DB 4; Length 426;
Best Local Similarity 99.1%; Pred. No. 9.9e-178;
Matches 420; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Y 1 MARRTPPDGNGRNVVLSAFPOSALVGVLSFGVFEFVAFAFEROARVWIASIGI 60
  |||
b 1 MARRTPPDGNGWVVVLSAFPOSALVGVLSFGVFEFVAFAFEROARVWIASIGI 60
  |||
Y 61 AVOQFSPVGSALSTKFGPRPVMTGIIAALGMLASFATSLTHLYLSIGLSSGML 120
  |||
b 61 AVOQFSPVGSALSTKFGPRPVMTGIIAALGMLASFATSLTHLYLSIGLSSGML 120
  |||
Y 121 TFAPTLACISCFPSRRSLATGALTGVLSFTFAPFOWMLSHVAMGSLIVSALS 180
  |||
b 121 TFAPTLACISCFPSRRSLATGALTGVLSFTFAPFOWMLSHVAMGSLIVSALS 180
  |||
Y 181 HUVACGALLRPSLSLEDDPAVGGPRAOTSLHNGPLRTVALTLINTGYFIPYHLVAH 240
  |||
b 181 HUVACGALLRPSLSLEDDPAVGGPRAOTSLHNGPLRTVALTLINTGYFIPYHLVAH 240
  |||
Y 241 LODLDWDLPAAFLLSVAILSDLVGRVVGMLGDAVPGVTFLLMLMTTLTGVSIALFPV 300
  |||
b 241 LODLDWDLPAAFLLSVAILSDLVGRVVGMLGDAVPGVTFLLMLMTTLTGVSIALFPV 300
  |||
/ ORGANISM: Homo sapiens
US-10-072-012-24
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Qy 301 AQAFTALVALAVANGFTSGALAPLAEVSLPELIGTRIRYCGLLQMIETISIGLGPPLS 360
  |||
Db 301 AQAFTALVALAVANGFTSGALAPLAEVSLPELIGTRIRYCGLLQMIETISIGLGPPLS 360
  |||
Qy 361 GYLKDVSNYTYASFVVGAFLLSGSGILLPLPHFECSTTTSGQDVLVTEALDTKVPPLPK 420
  |||
Db 361 GYLKDVSNYTYASFVVGAFLLSGSGILLPLPHFECSTTTSGQDVLVTEALDTKVPPLPK 420
  |||
Qy 421 EGLE 424
  |||
Db 421 EGLE 424
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RESULT 11
US-10-072-012-24
/ Sequence 24, Application US/10072012
/ Publication No. US20040033493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zethusen, Bryan
/ APPLICANT: Patuturajan, Meera
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 447
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-24
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[illegible]

PRIOR APPLICATION NUMBER: PCT/US02/05064
 PRIOR FILING DATE: 2002-02-21
 PRIOR APPLICATION NUMBER: 60/270,658
 PRIOR FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: 60/304,444
 PRIOR FILING DATE: 2001-07-12
 NUMBER OF SEQ ID NOS: 445
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 224
 LENGTH: 142
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-644-807-224

Query Match 30.2%; Score 704; DB 5; Length 142;
 Best Local Similarity 99.3%; Pred. No. 4.1e-53;
 Matches 139; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

285 MWTTLTGVSALFPVAQAPTAVALAVAGFTSGALAPLAFSVLPBELIGTRRIYCGGL 344
 1 MWTTLTGVSALFPVAQAPTAVALAVAGFTSGALAPLAFSVLPBELIGTRRIYCGGL 60
 345 LQWIESIGLGLGPPLSGYLRDVSGNTASRVVAGAPLLSSGILLTLPHFFCSTTTSGP 404
 61 LQWIESIGLGLGPPLSGYLRDVSGNTASRVVAGAPLLSSGILLTLPHFFCSTTTSGP 120
 405 QDLVTEALDTKVPPLPKEGLE 424
 121 QDLVTEALDTKVPPLPKEGLE 140

RESULT 14
 US-10-644-807-314

Sequence 314, Application US/10644807
 Publication No. US20060057582A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 83 Human Secreted Proteins
 FILE REFERENCE: PS/735
 CURRENT APPLICATION NUMBER: US/10/644,807
 CURRENT FILING DATE: 2003-08-21
 PRIOR APPLICATION NUMBER: PCT/US02/05064
 PRIOR FILING DATE: 2002-02-21
 PRIOR APPLICATION NUMBER: 60/270,658
 PRIOR FILING DATE: 2001-02-23
 PRIOR APPLICATION NUMBER: 60/304,444
 PRIOR FILING DATE: 2001-07-12
 NUMBER OF SEQ ID NOS: 445
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 314
 LENGTH: 142
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-644-807-314

Query Match 30.2%; Score 704; DB 5; Length 142;
 Best Local Similarity 99.3%; Pred. No. 4.1e-53;
 Matches 139; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

285 MWTTLTGVSALFPVAQAPTAVALAVAGFTSGALAPLAFSVLPBELIGTRRIYCGGL 344
 1 MWTTLTGVSALFPVAQAPTAVALAVAGFTSGALAPLAFSVLPBELIGTRRIYCGGL 60
 345 LQWIESIGLGLGPPLSGYLRDVSGNTASRVVAGAPLLSSGILLTLPHFFCSTTTSGP 404
 61 LQWIESIGLGLGPPLSGYLRDVSGNTASRVVAGAPLLSSGILLTLPHFFCSTTTSGP 120
 405 QDLVTEALDTKVPPLPKEGLE 424
 121 QDLVTEALDTKVPPLPKEGLE 140

ESULT 15

US-09-829-432-4
 Sequence 4, Application US/09829432
 Publication No. US20030166522A1
 GENERAL INFORMATION:
 APPLICANT: KETCHUM, Karen et al.
 TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
 NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
 AND USES THEREOF
 FILE REFERENCE: CL001013
 CURRENT APPLICATION NUMBER: US/09/829,432
 CURRENT FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 09/815,301
 PRIOR FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: 60/254,554
 PRIOR FILING DATE: 2000-12-12
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 456
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-09-829-432-4

Query Match 27.7%; Score 645; DB 3; Length 456;
 Best Local Similarity 36.1%; Pred. No. 2.4e-47;
 Matches 170; Conservative 70; Mismatches 193; Indels 38; Gaps 9;

3 RTEPPDGGWRVAVVLSAFQSAIVFGVRSFGVFEVFAAEEQAAVSMASIGIAV 62
 1 RGAPPDGGWGVVLSAFQSAIVFGVRSFGVFEVFAAEEQAAVSMASIGIAV 60
 63 QQFSPVGSALSTFYGPRPVMTGAILAALGMLASFATSLTHLYSLGSSGMALTF 122
 61 LYTGCPILSLVTRFGCRPVVLAAGLLASACMLTASRSRLLELYTAGVLTGLALNF 120
 123 APTLACISCTFSRRRSIATGIALTVGLSFTFAPFOWMLSHYAMRGSLLVGSLSHL 182
 121 QPSLIMGLYFERRRRPLANGIAAGSPVFLSTLPLQLGGERGWRGGLPGGLLHC 180
 183 VACGALRPPSLAE--DPAVGPRAQLTSLH----HGPELYTVALTLINTGYEIPY 234
 181 CACGAVWRPPPGQPPDPAPPGRARHRLDLAVCTDRTFMVMTKFLMALGLFVPA 240
 235 LHVVAHQDLDMDPLPAFLSLVVAISDLVGRVVG---WLGDAVGPVTRLLMNTTLT 291
 241 ILVNVAKADGAVDDEAFLLSIVGEVDIVARPACALAGLGRLP-HVYLFSLALLAN 299
 292 GVSALFPVAQAPTAVALAVAGFTSGALAPLAFSVLPBELIGTRRIYCGILLQWIESI 351
 300 GLTDLISARARSYGLTVAFCIAFGLSYGMVGAIOFEVLNAVTCARPFPASGLVLAENV 359
 352 GGLGPPLSGYLRDVSGNTASRVVAGAPLLSSGILLTLPHFFCSTTT-----400
 360 AVLIGPSPAGRLVDLAKYETIFFYLAGS-EVALAGVMAVITTYCCRCRCKNISGRSAEG 418
 401 -TSGPDVTEALDTKVPPLPKEGLEGUNSTESGPESQSLTAPGLLPLTG 450
 419 GASDPEDEV--EAERDESEMPA-----STE---EPGSLAEVLSPRAG 456

Search completed: September 7, 2006, 13:12:06
 Job time: 184 secs

301 AQAFTALVALVAGFTSGALAPLAFSVLPPELLIGTRRIYCCGLHLOWIESIGGLGPPLS 360
 315 ACIDYGLVVFICFIFGICSGWNGALQFELVMAIVGTHNFSSALIGVLMEAVAVLVGPSSG 374
 361 GYLNDVSGNVTASVAVAGAFLLSSGILLTLPHFFCSTTTSGQDLYTEALDTKVLPL 419
 375 GKLLDATHVYVYFVLGAEVLTSSLILL--LGNFFCIRKKPEQPEVMAAEEBKLRHP 432

RESULT 2
 5-10-530-837-8
 Sequence 8, Application US/10530837
 Publication No. US20060168670A1
 GENERAL INFORMATION:
 APPLICANT: LG Life Sciences Ltd.
 TITLE OF INVENTION: Gene Families Associated With Cancers
 FILE REFERENCE: IL03PCT006
 CURRENT APPLICATION NUMBER: US/10/530,837
 PRIOR FILING DATE: 2005-04-08
 PRIOR APPLICATION NUMBER: US60/419911
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: US60/419912
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: US60/420088
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: US60/434243
 PRIOR FILING DATE: 2002-12-16
 PRIOR APPLICATION NUMBER: US60/434278
 PRIOR FILING DATE: 2002-12-16
 PRIOR APPLICATION NUMBER: US60/438278
 PRIOR FILING DATE: 2003-01-03
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: Knapentin 1.71
 SEQ ID NO: 8
 LENGTH: 477
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-10-530-837-8

Query Match 16.6%; Score 386.5; DB 6; Length 477;
 Best Local Similarity 24.1%; Pred. No. 5e-22;
 Matches 116; Conservative 76; Mismatches 150; Indels 139; Gaps 10;

6 PDGCGRRVVLASAFQSAVFGVLSFGVFVEFVAEFEOARVSIASIGIAVQPGS 67
 7 PDGCGWYIVFVYSLTQFLCTGSLAVGLYEMLDATGEGKKAWSGLASVGLIAS 66
 68 PVGSALSTRKFGPRPVMTGILALGMLASPAFSLTHLYLSIGLSSGMAITFAPTLA 127
 67 PVCSLCVSSFGARVPTIFSGFMVAGMLMSFAPNIYFLFYSYIVGS----- 115
 128 CLSCFSRRRLATGALTGVLSSFTAFPFQWLLSHYARGLLYSALSILHVAAGA 187
 116 -----SVGL--FTYALQRMVVERFYGLDGLLIGALALNITLACGS 154
 188 LLRPSLAEDPA-----VGGPRAQLT----- 208
 155 LMRPLQSSDCLPKKIVADEDLDPKYSIYNEKGNLENIINILDKSYSEKCRITLANGD 214
 209 -----SLHNGPRLKRT----- 220
 215 WKQDSLHKNPVTHTKPEDEYTKKVAEQTTFCKGLARKKQOLYKNGCFEVALFKXKVF 274
 221 ---VALTLINTGYEIPYLHT--VAHLODLMDP--LPAAFLSSVAISDLVGRVSGWL 272
 275 SALFIALILFDIGCFPPSLMEDVARSSNVKEEFIMP---LIITIGIMTAVGKLLGIL 331
 273 GDAVGPVTRLLMTTTLTGVSALFPVAOAPVALVAVAGFSGSGLAFLASVLP-- 330
 332 ADFKMINILYLVALLIMGLALCAIPFAKSVTTLALISGLIGFTG-----NMSIFPV 386
 331 --ELICTRRIRYCGI GULQMTESIGGLGPPLSGYRDNVSGNVTASVAVAGAFLLSSGIL 388

387 TTKTVGIEKLAAHYGILMFPAAGLNSLQPLIVGFYMTQYTDIAFYFSRGCYVLGGRTL 446
 389 L 389
 447 L 447

RESULT 3
 US-11-251-208-168
 Sequence 168, Application US/11251208
 Publication No. US20060137043A1
 GENERAL INFORMATION:
 APPLICANT: Puzio, Piotr
 APPLICANT: Chardonnens, Agnes
 APPLICANT: Shirley, Amber
 APPLICANT: Wang, Xi-Qing
 APPLICANT: Sarria-Millan, Rodrigo
 APPLICANT: McKersie, Bryan
 APPLICANT: Chen, Ruoying
 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
 TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
 TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
 FILE REFERENCE: 13311-00015-US
 CURRENT APPLICATION NUMBER: US/11/251,208
 PRIOR FILING DATE: 2005-10-14
 PRIOR APPLICATION NUMBER: PCT/US2004/011888
 PRIOR FILING DATE: 2004-04-15
 PRIOR APPLICATION NUMBER: EP 03008080.8
 PRIOR FILING DATE: 2003-04-15
 PRIOR APPLICATION NUMBER: EP 03009728.1
 PRIOR FILING DATE: 2003-05-02
 PRIOR APPLICATION NUMBER: EP 03016772.2
 PRIOR FILING DATE: 2003-08-01
 PRIOR APPLICATION NUMBER: EP 03022225.1
 PRIOR FILING DATE: 2003-09-30
 NUMBER OF SEQ ID NOS: 852
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 168
 LENGTH: 673
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 US-11-251-208-168

Query Match 10.1%; Score 236; DB 7; Length 673;
 Best Local Similarity 24.5%; Pred. No. 2.4e-10;
 Matches 107; Conservative 69; Mismatches 213; Indels 48; Gaps 14;

7 PPDGNGRRVVLASAFQSAVFGVLSFGVFVEFVAEFEOAR--VSWIASIGIAVO 63
 206 PPDGCGWVTVFCVFLPMTSGCNASFGVDLAYVILNDTYPGASKYDIALIAGLTVEFG 265
 64 QCGSPVGSALSTRKFGPRPVMTGILALGMLASPAFSLTHLYLSIGLSSGMAITF 123
 266 QLLSPVWMLKRIIGRTTLMFGDAVMLAAYLASFTTKLMQOLYTOGFMWGSISLIFV 325
 124 PTLACLSYFSRRRLATGALTGVLSSFTAFPFQWLLSHYA--WRGSLLVASLSL 180
 326 PATTVLPQWFLKKRAVAGVSLTGAGGVVYGLATNMKLSDFGNTRMCLRIIGISC-SI 384
 181 HLVACGALL--RPSLAEDPAVG--GPPAQLTSL-----LHNGP-----LRYTVALT 224
 385 SVLVAILALKENPT---PAIGLSPRAAMEQLAMSLKVTITPEFVLLALMMPALF 440
 225 LINTGYEIPYLHVAH--LODLMDPLPAAFLSSVAISDLVGRVSGWLGDVPGPVTRL 283
 441 ANNMWFTLSSYAISKGLSSHD-----ASTLTAIINGQSIGRPLMGADKDF--GRANVT 494
 284 LMLMTTTLTGVSALFPVAOAPVALVAVAGFSGSGLAFLASVLPPELLIGTRRI----- 338
 495 IYVTLTTLITTYMFAFNIIPATTFVQLIFFSILVOSCVGVANNVTVLIDAMVNRDEEPLPAMA 554
 339 ---YCGLGLLOWIESIGGLGPPLSGYRDNVSGNVTASVAVAGAFLLSSGILLTLPHFF 395


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; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48618
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48618

Query Match      6.4%; Score 150; DB 6; Length 591;
Best Local Similarity 22.9%; Pred. No. 0.00077;
Matches 99; Conservative 64; Mismatches 161; Indels 108; Gaps 20

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Query Match Similarity 6.4%; Score 150; DB 6; Length 591;
Best Local Similarity 22.9%; Pred. No. 0.00077;
Matches 99; Conservative 64; Mismatches 161; Indels 108; Gaps 20;

QY 26 LVFGVLSFGVFVEFVAABEEOARVS-WIASIGIAY----QQFGSVGSALST--KF 77
 ::: :
Db 85 LAIAAANLGGYLMLYSTVGSRGVARCPPELVLCYLIAGANSQAFAINT--GALTVCVNRF 142

[illegible]


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/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: Pfam Name: Sugar_tr; Pfam Description: Sugar (and other)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 42569720; NR Description: transporter-related
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 34908356; NR Description: P0529H1.31 [Oryza
/ OTHER INFORMATION: sativa (japnica cultivar-group)] >gi|16461191|dbj|BAB84388.1|
/ OTHER INFORMATION: P0529E05.3 [Oryza sativa (japnica cultivar-group)]
/ OTHER INFORMATION: >gi|20805189|dbj|BAB92858.1| P0529H1.31 [Oryza sativa (japnica
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 51536596; NR Description: A13g46980 [Arabidopsis
/ OTHER INFORMATION: thaliana] >gi|22331630|ref|NP_190282.2| transporter-related
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 42572593; NR Description: transporter-related
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: GI Number: 56784504; NR Description: putative membrane
/ OTHER INFORMATION: glycoprotein Hp59 [Oryza sativa (japnica cultivar-group)]
/ OTHER INFORMATION: >gi|56784255|dbj|BAD81937.1| putative membrane glycoprotein Hp59
/ US-11-174-307B-3218
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Query Match 6.3%; Score 147; DB 7; Length 529;
Best Local Similarity 21.3%; Pred. No. 0.0012;
Matches 105; Conservative 60; Mismatches 173; Indels 154; Gaps 22;
```

```
11 GW-----GRVVVSAFPQSALVFCVLSFGVFVEFVAFEQARVSWIAS----- 57
76 GWRARRRGCREVNAEC---$ASLGGVRHGAALAAVPSVPALPERAKVVAALVAAMLCNA 132
58 -----IGIAVOQ-----FGSPVGSALSTFKGPRPVMTGIL 89
133 DRVAVSAVAVVPLAAQHGSSSFVGIYQSSFLMGVVFSSMVGALADRYGKKVAGAAAL 192
90 AALGMLASPATSLT-HLYSLIGLSSGWAALTFAFLACLCYF-SRRSLATGLALTG 147
193 WSLATFLTPMAASQASATMLLAVERLFGVABGVAFPPTWSTFLPKWFPHERATAVGLSMG 252
148 VGLS---SFTFAFFQWLLSH-----YAMRGSLL-----VSALS 179
253 FHLGNVSVFLATPI---IMSHIGLAGTFAFFASLGIYLSVWMLNVEDSPIDSRITSKE 309
180 LHLVACGALLRPSLAEDPAVGGPRAQLTSLHHGPFLLRTVALTLINTGYFI-----P 233
310 LQILLAGR-----SKSYKVGKSPSLREVFSKEMWMAIIVANVINNMGYFLLSMFV 362
234 YHLV--AHKQDLW--DLP-----AFL-----LSVAISDLGVVSGWL 272
363 YKTYVNVNVLKQANFSAIPKGMALSGVAGASADFMKISGLSIYRVAKINGSI--GFI 420
273 GDVAPGPTRLMLMTTLTGVSALFPVAQAPT-ALVALAVYCGTSGALAPLASV--- 328
421 G-----PGVSLCLCFRAQTBSAAAVMTAALGSSCSQAGYFCNVDDI 463
329 LPELIGTRIRYCGILQMIISIGLGLPPLSGYLRDVSGNTYASFVAGAFLLSGSGL 388
464 APKVAAGSLH-----GNTNGIGTVAIVASTVGAGYFVQWLGSGFOA-----F 503
389 LTLPHFFCFSTT 400
504 LTLTAVLVFSAT 515
```

:SULT 9

```
US-11-274-317A-2
/ Sequence 2, Application US/11274317A
/ Publication No. US2006017912A1
/ GENERAL INFORMATION:
/ APPLICANT: FARWICK, Mike
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE dep34 GENE
/ FILE REFERENCE: 032301MD203
/ CURRENT APPLICATION NUMBER: US/11/274.317A
/ PRIOR FILING DATE: 2005-11-16
/ PRIOR APPLICATION NUMBER: US/09/946,763
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 549
/ TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
/ US-11-274-317A-2
```

```
Query Match 6.0%; Score 140.5; DB 7; Length 549;
Best Local Similarity 21.3%; Pred. No. 0.0038;
Matches 105; Conservative 61; Mismatches 199; Indels 127; Gaps 17;
```

```
QY 13 GRVVVSAFPQSALVFCVLS-----FGVFVEFVAFEQARVSWIASIGIAVOQFG 66
DB 45 GRV-----GFIILMLMLLSLQGITFGSALPTIVGEL-GVVMHMTVITAFLLGQTI 99
QY 67 SPVGSALSTFKGPRPVMTGIIAAGMLASPATSLTHLYSLIGLSSGWAALTFAPTL 126
DB 100 LPIFGKLGDPFGKRYLFMFPAIAPVVGSIIGALAQNNVTILIVARALQGIAGGLMISQA 159
QY 127 ACISCFRRSLATGLALTGVLSSFTFAFPFQWLLSHYAMRGSLL-VSALSILHYAC 185
DB 160 ITADVTTARERAKYMGIMGSVFLSSILGPIGLGWTDEGMRGMLNVPDGIITLVAI 219
QY 186 GALLRPP-----SLAEDPAV-----GGPRAQLTSLHHGPFLLRTVA 222
DB 220 AVLLKLPANERGVSVDMGSIEMAIATTAFAVLAVTWGNEVEMASPMIIGLFTLLVAA 219
QY 223 -----LTLINTGYFI-YLHLVAHLQDID 245
DB 280 IVFVFEKRAVDPIVPMGLFSNRNFVLTAVAGIGVGLFMWGTAIVPTLYQVHGLNPTQ 339
QY 246 WDPLEPAFLSVVAISDLGVVVS-----GWLGDVAPGVTLLMNTTLTGVSAL 297
DB 340 AGIAMLIPMMIGLIGSTVGNIVSKTKYKWPFIQMLI--MVALVLVLTSLT----- 390
QY 298 PVAQAPTALVALAVYCGTSGALAPLASVLP-----ELIGTRIRYCGILQMI 348
DB 391 -----PASLALIGLYFVFVGFGICAMQILVLIVQNSPITWGT-----ATSSNNF 439
QY 349 ESIGGLPPLSG--YLADVSANT-----ASFVAGALFLSG-----SGILLTPHFF 395
DB 440 RQIGAVGSALIGLGLFISLSDRFTENVPAAVASMGEEAGYASMSDFSGASNLTPHL- 498
QY 396 CFSITTSQPD 407
DB 499 -----VESLPOAL 506
```

RESULT 10

```
US-11-296-657-3
/ Sequence 3, Application US/11296657
/ Publication No. US20060143736A1
/ GENERAL INFORMATION:
/ APPLICANT: Schneberger, Richard, Margolles-Clark, Emilio, Park, Joon-Hyun,
/ TITLE OF INVENTION: MODULATING PLANT CARBON LEVELS
/ FILE REFERENCE: 11696-149001
/ CURRENT APPLICATION NUMBER: US/11/296,657
/ CURRENT FILING DATE: 2005-12-06
/ NUMBER OF SEQ ID NOS: 100
/ SEQ ID NO 3
```

LENGTH: 508
TYPE: prt
ORGANISM: Populus tremula x Populus tremuloides
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(508)
OTHER INFORMATION: Public GI no. 57283317
-11-296-657-3

Query Match 6.0%; Score 140; DB 7; Length 508;
Best Local Similarity 23.0%; Pred. No. 0.0038;
Matches 113; Conservative 62; Mismatches 199; Indels 118; Gaps 24;

```
42 VAAFEQARVSMVSIAGIAVQFGSP-----VGS-----71
|||
35 VAAPIHRAFHLSWSPFACFVSSFAAPLLPIIRDNLNTASDIGNAGIASVGAVFARV 94
|||
72 ALSTR---FGPRPVMTGILALGMLASFATSLHLVLSGLSGSGMALTPATLAC 128
|||
95 AMGTACDLFGPRIASASLILTPAPAVYFTSMASSTS--FLVRFPTGSLA-TFVSTQFW 152
|||
129 LSCYFS-----RRSLATGLALTGVLSFTFAPFPQWL-----LSHYAMRGSLLVSL 178
|||
153 MSMSAPVVTGANGVAGGWNLGAGATQIIMPVYGLIRDIGAIKFTAMR-IAFFIRPL 211
|||
179 SLHLVACGALLRPPSLAE-----DPAVGGPRAQLTSLHGPFLR-----218
|||
212 FQTLASFVAVLIFGKDLDPGNFRRLQKAGDKTKDKFSNVFYHG--IKVYRGWILASVGYC 269
|||
219 YVALTLIN--TCYTFPYLHVLAHLODLDMPLEPAFLISVAISDLVGRVVSGLMGDAV 276
|||
270 FVEVLTIDIVAEFYDRFDLKLH-----TACMIASGLANIVSRPGGMIISDAV 320
|||
277 P--GPVTRLLMLMT--TLTGV-SLALFPVAQPTALVALAVAGTSGALAPLAFVLP 330
|||
321 GRFGMRGKLTMLMVQTLIGVFCILGRVSLGASIVMIVPELFCQAACG-LFPGVVP 379
|||
331 ELIGTRRITCGICLLOMISIGLGLPPLSGVLRDVSGNTASFVVAAGFLISGGLILT 390
|||
380 FV--SRR--SLGLISGMTGGGNGVAVLTQLIFFRGSXYKXK--RGIMLGVMILCCT 431
|||
391 L-----HF-----FCFSTTSGQDLVTEALDTKPLKREGLEGD-----NST 430
|||
422 LITCLIHFPQWGMFCGSPSTK---IATBEDYYSSEMNSEKELHLISLKPDNSKS 487
|||
431 ESGPESQSLTAP 442
|||
488 ERGRKEDSETRP 499
```

RESULT 11
S-11-056-355B-83755
Sequence 83755, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 83755
LENGTH: 550
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(550)
OTHER INFORMATION: Ceres Seq. ID no. 12671665

US-11-056-355B-83755
Query Match 5.9%; Score 138; DB 7; Length 550;
Best Local Similarity 22.1%; Pred. No. 0.0059;
Matches 85; Conservative 42; Mismatches 114; Indels 144; Gaps 16;

```
106 LYLSTGLSSGMAITFAPTLACSCY--FSRRSLATGLALTGVGSSFTFAPFPQWL 163
|||
90 LYICIGANSON-----FANTGALVTCVKNPESRGVNLGKGVGSLGALFTQLYFAIY 144
|||
164 SH-----YAW-----RGSLL-----LVSA-LSHLVA---184
|||
145 GHDSKSLILLIAMLPAVSLVFYLLIREKKVVRQNELSVFYQFLVYSIFLALFLMAMNI 204
|||
185 -----CGALLRP-----192
|||
205 AEQVHFSKAAVASATICCALLFVPLTVSVKOLEVWMMKPLIEBPSEVKYKPKEL 264
|||
193 SLADPA--VGGPRAQLTSLH--HGPELR--YVALTLINTGYFIPYHLVAHL-----241
|||
265 DLDQDKAKVNGEERKYSCTVFSPPRGEYTILOALISTDMITLFFVATFCGLSSSL 324
|||
242 -----QDLMDPLPAFLSVVAISDLVGRVVSGLMGD-----AVGPVTRLLM 285
|||
325 TAVNNTQIGESLGYPNHTVSSFSVLSVIMNYRGRVSGFVSEYLLAKYKLPRLIMMTLV 384
|||
286 LMTTLTVSIALFPVAQPTALVALAVAGFTSGALAPLAFSVPELIGTR---RIYCG 341
|||
385 LLSLCAGHLIAFPV---PGSVYIASILMGFSFGAQLPLFAISDELFGKLYSTLPNC- 440
|||
342 LGLIOMIESIGLGLPPLSGVLRDV 366
|||
441 -----GQLASPLGSTITLVN 454
```

RESULT 12
US-11-056-355B-83754
Sequence 83754, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 83754
LENGTH: 558
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(558)
OTHER INFORMATION: Ceres Seq. ID no. 12671664
US-11-056-355B-83754

Query Match 5.9%; Score 138; DB 7; Length 558;
Best Local Similarity 22.1%; Pred. No. 0.006;
Matches 85; Conservative 42; Mismatches 114; Indels 144; Gaps 16;

```
106 LYLSTGLSSGMAITFAPTLACSCY--FSRRSLATGLALTGVGSSFTFAPFPQWL 163
|||
98 LYICIGANSON-----FANTGALVTCVKNPESRGVNLGKGVGSLGALFTQLYFAIY 152
|||
164 SH-----YAW-----RGSLL-----LVSA-LSHLVA---184
|||
153 GHDSKSLILLIAMLPAVSLVFYLLIREKKVVRQNELSVFYQFLVYSIFLALFLMAMNI 212
|||
185 -----CGALLRP-----192
```


Best local similarity 21.0%; Pred. No. 0.0062;
Matches 98; Conservative 82; Mismatches 156; Indels 131; Gaps 24;

```
Y 26 LTFGV--LRSGVFVEFVAFAFEQAAVSWIASIGIAVQGFSPVGSAL---STKFG 78
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 18 LTFGYDTGVISGAILFI-----OKQMNIGSWQGWVSAVLIGAILGAILIGPSSDRFG 71
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Y 79 PRPVVATGGLAALGMLASFATSLTHLYS---IGLSSGWAL--TFAPTLACLSCYF 133
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 72 RRTLLLSALIFVVGALGSASFPEFWTLISRIILGNVAGASALIPYIALAP----- 126
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Y 134 SRRSLATGL---ALTGVL---SSETFAPPF--QMLISHYAMRGSLILVSALSLLHY 183
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 127 SDRGTVSSILFQLMVMTGILLAYITNYSFSGFYTGWRMMLGFAAIPALILFL----- 178
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Y 184 ACGALLRPPSLADDPVAGGPRAOULTSLHHGPFLRYVALTLINTGYFIPLYHLVAHLQD 243
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 179 --GGLILPES-----PR-----FLVKSGLDEARHVLDTMVK 208
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Y 244 LDWDPPLPAFPLLSVAISDLVGRVSGMLGDVAPGPTRLMLMTLLTGVSLALFP----- 299
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 209 HD---OVAVNKEINDIQESAKIVSGW--SELFGRVVRP---SLIGIGLAIFOQVMG 258
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Y 300 ---VAQAPTALVALAVAGFTSGALAPLSV-----LPELIGTRRIY---C 340
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 259 CNTVLVYVAPT--IFTDVGFGVSALLAHIGIFNVIVTAIAVAIMDKIDRKKIWNIGAV 316
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Y 341 GILGLQWIEISIGILGPPPLSGYLRDVSGNYTASFVAVAGAFLLSGGILLTLPHPFCESTF 400
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 317 GMGISLFWMSIG-----MKFSGGSOTPAIT-----SVTALIV--YIAFSA 355
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Y 401 TSGPDVLVTEALDTKVPPLPKKEGLEGLNSTESGPESQ--SLTAPGLL 445
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
b 356 TWGP--VMMWMIQEVFPPLNIRGLGNFASVYNMTANNIVSLTFPSLL 400
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
```

Search completed: September 7, 2006, 13:12:46
Job time : 37 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocelebration Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2006, 12:58:21 ; Search time 196 Seconds

(without alignments)
1066.061 Million cell updates/sec

Title: US-10-654-428-2

Sequence: 1 MARRTPPPGGMGRVVVLSA.....SLTAPGLLPRLGLHRTVP 457

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2331	100.0	457	5	ABG30739
2	2323	99.7	457	5	ABP68801
3	2323	99.7	458	5	ABP68801
4	2154	92.4	426	5	ABP61019
5	2151	92.3	426	5	ABP61019
6	2150	92.2	426	5	ABG32785
7	2150	92.2	426	5	AD116770
8	2143	91.9	426	10	ABG13486
9	2142.5	91.9	427	5	ADN42424
10	2142.5	91.9	427	5	AD116802
11	2142.5	91.9	427	5	AD117243
12	2142	91.9	426	5	AD116766
13	2142	91.9	426	5	AD116766
14	2142	91.9	426	8	ADN42420
15	2142	91.9	426	8	ADN42422
16	2142	91.9	426	10	ABG13482
17	2142	91.9	426	10	ABG13484
18	2142	91.9	426	10	ABG13484
19	941	40.4	186	4	AAU01618
20	930.5	39.9	447	5	ABB80595
21	930.5	39.9	447	5	AD116488
22	930.5	39.9	471	4	AAU93737
23	930.5	39.9	471	8	AD131672

24	920	39.5	472	5	AD116494	Ad116494 Human NOV
25	911	39.1	472	8	ADN42150	Adn42150 Human nov
26	900.5	38.6	447	8	ADN42144	Adn42144 Human nov
27	704	30.2	142	5	ADG79418	Adg79418 Human sec
28	704	30.2	142	5	ADG79508	Adg79508 Human sec
29	643	27.6	290	5	AD117855	Ad117855 Human NOV
30	640	27.5	486	6	AAO27118	AAO27118 Monocarob
31	637.5	27.3	486	5	AAE22711	AAE22711 Monocarob
32	637.5	27.3	486	6	AAO27116	AAO27116 Monocarob
33	637.5	27.3	516	6	AAE22913	AAE22913 Human tra
34	637.5	27.3	516	6	AAO27117	AAO27117 Monocarob
35	637.5	27.3	516	6	AAO27119	AAO27119 Monocarob
36	634.5	27.2	486	6	AAO27119	AAO27119 Monocarob
37	634.5	27.2	486	8	ADR09111	ADR09111 Human pro
38	630	27.0	308	5	ABE80594	ABE80594 Human sbg
39	630	27.0	308	5	AAE21157	AAE21157 Human TRL
40	625.5	26.8	504	8	ADN29577	ADN29577 Human mon
41	625.5	26.8	504	8	AEA35823	AEA35823 Human mon
42	625.5	26.8	513	9	ADN29613	ADN29613 Strept-tag
43	625.5	26.8	513	9	AEA35859	AEA35859 Human mon
44	619.5	26.6	375	4	AAE88570	AAE88570 Human hyd
45	617	26.5	489	5	AD116804	AD116804 Rat NOV

ALIGNMENTS

RESULT 1
ABG30739
ID ABG30739 standard; protein; 457 AA.
XX
AC ABG30739;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human monocarboxylate transporter related polypeptide.
XX
KW Human; transporter; gene therapy; monocarboxylate transporter.
XX
OS Homo sapiens.
XX
PN WO200248364-A2.
XX
PD 20-JUN-2002.
XX
PF 11-DEC-2001; 2001MO-US047557.
XX
PR 12-DEC-2000; 2000US-0254554P.
PR 23-MAR-2001; 2001US-00815301.
PR 10-APR-2001; 2001US-00829432.
XX
PA (PEKE) BE CORP NY.
XX
PI Ketchum KA, Webster M, Merkulov G, Di Francesco V, Beasley EM;
XX
DR WPI; 2002-563516/62.
XX
PS N-PSDB; ABE89371.
XX
PT Transporter proteins related to the monocarboxylate transporter
PT subfamily, for diagnosing and treating diseases mediated by the
PT transporter protein and identifying modulators.
XX
PS Claim 1; Fig 2A; 84pp; English.
XX
CC The invention relates to a human transporter protein and the
CC polynucleotide encoding it. The protein is useful for identifying a
CC modulator of the expression of the peptide by contacting the peptide with
CC an agent and determining if the agent has modulated the function or
CC activity or expression of the peptide. The sequences are useful as models
CC for the development of human therapeutic targets, aid in the
CC identification of therapeutic proteins and serve as targets for the
CC development of human therapeutic agents that modulate transporter
CC activity. The transporter proteins also provide a target for diagnosing a

disease or predisposition to a disease mediated by the protein, in a pharmacogenomic analysis and for treating disorders characterized by an absence of inappropriate or unwanted expression of the protein. This sequence represents a human transporter protein, related to the monocarboxylate transporter subfamily

Sequence 457 AA:

Query Match 100.0%; Score 2331; DB 5; Length 457;

Best Local Similarity 100.0%; Pred. No. 1.4e-205; Mismatches 0; Indels 0; Gaps 0;

Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MARRTEPPDGGMGWVVLAFPOSALVFGLRSFGVFEEFVAAREEQARVSWIASIGI 60
1 MARRTEPPDGGMGWVVLAFPOSALVFGLRSFGVFEEFVAAREEQARVSWIASIGI 60
61 AVOQFGSPVGSALSTKFGPRPVMTGGIILALGMLASFATSLTHLYLSIGLSSGGMAL 120
61 AVOQFGSPVGSALSTKFGPRPVMTGGIILALGMLASFATSLTHLYLSIGLSSGGMAL 120
121 TFAPTLACLSCYFSRRSLATGLATGVLSFTFAPFPQMLSHYAMGSLILVSAISI 180
121 TFAPTLACLSCYFSRRSLATGLATGVLSFTFAPFPQMLSHYAMGSLILVSAISI 180
181 HLVACGALLRPPSLAEDPAVGGRPAQQLTSLHHGFLRYVALTLINTGYFIPLYLVAH 240
181 HLVACGALLRPPSLAEDPAVGGRPAQQLTSLHHGFLRYVALTLINTGYFIPLYLVAH 240
241 LODLMDPLPAFLSLVVAISDLVGRVSGMLGDVAPGPTLLMWTLLTGVSILAFPV 300
241 LODLMDPLPAFLSLVVAISDLVGRVSGMLGDVAPGPTLLMWTLLTGVSILAFPV 300
301 AQAFTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLGPPLS 360
301 AQAFTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLGPPLS 360
361 GYLKRVSGNTTASFAVAGAFLLSSGILLTLPHFCFSTTSGPQDLVTBALDTKVP LK 420
361 GYLKRVSGNTTASFAVAGAFLLSSGILLTLPHFCFSTTSGPQDLVTBALDTKVP LK 420
421 EGLEGLNSTESGPESQSLTAPGLLPRLGLHRTTVP 457
421 EGLEGLNSTESGPESQSLTAPGLLPRLGLHRTTVP 457

RESULT 2
ABP69801 standard; protein: 457 AA.
ABP69801:
20-JAN-2003 (first entry)
Human polypeptide SEQ ID NO 1848.
Human: genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytotoxic; immunomodulator; nocotropic; neuroprotective;
antiParkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
antiarthritis.
Homo sapiens.
WO200270539-A2.
12-SEP-2002.
05-MAR-2002; 2002MO-US005095.
05-MAR-2001; 2001US-00799451.

(HXSE-) HXSEQ INC.
Tang YF, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F,
Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,
Wehrman T, Wang J, Wang D, Drmanac RT,
WPI: 2002-759812/82.
DR N-PSDB: AB212018.
DR N-PSDB: AB212018.
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
PS Claim 9; SEQ ID NO 1848; 1012pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (1) comprising a
nucleotide sequence selected from any of 948 sequences (AB21119-
AB212066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for
identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP69802-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, liver
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 457 AA;

Query Match 99.7%; Score 2323; DB 5; Length 457;

Best Local Similarity 99.8%; Pred. No. 7.8e-205; Mismatches 1; Indels 0; Gaps 0;

Matches 456; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MARRTEPPDGGMGWVVLAFPOSALVFGLRSFGVFEEFVAAREEQARVSWIASIGI 60
1 MARRTEPPDGGMGWVVLAFPOSALVFGLRSFGVFEEFVAAREEQARVSWIASIGI 60
61 AVOQFGSPVGSALSTKFGPRPVMTGGIILALGMLASFATSLTHLYLSIGLSSGGMAL 120
61 AVOQFGSPVGSALSTKFGPRPVMTGGIILALGMLASFATSLTHLYLSIGLSSGGMAL 120
121 TFAPTLACLSCYFSRRSLATGLATGVLSFTFAPFPQMLSHYAMGSLILVSAISI 180
121 TFAPTLACLSCYFSRRSLATGLATGVLSFTFAPFPQMLSHYAMGSLILVSAISI 180
181 HLVACGALLRPPSLAEDPAVGGRPAQQLTSLHHGFLRYVALTLINTGYFIPLYLVAH 240
181 HLVACGALLRPPSLAEDPAVGGRPAQQLTSLHHGFLRYVALTLINTGYFIPLYLVAH 240
241 LODLMDPLPAFLSLVVAISDLVGRVSGMLGDVAPGPTLLMWTLLTGVSILAFPV 300
241 LODLMDPLPAFLSLVVAISDLVGRVSGMLGDVAPGPTLLMWTLLTGVSILAFPV 300
301 AQAFTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLGPPLS 360
301 AQAFTALVALAVAGFTSGALAPLAFSVLPBLIGTRRIYCGILQMTESIGLGPPLS 360
361 GYLKRVSGNTTASFAVAGAFLLSSGILLTLPHFCFSTTSGPQDLVTBALDTKVP LK 420
361 GYLKRVSGNTTASFAVAGAFLLSSGILLTLPHFCFSTTSGPQDLVTBALDTKVP LK 420
421 EGLEGLNSTESGPESQSLTAPGLLPRLGLHRTTVP 457
421 EGLEGLNSTESGPESQSLTAPGLLPRLGLHRTTVP 457

RESULT 3
ABB80596
ID ABB80596 standard; protein; 458 AA.
XX
XX AC
XX ABB80596;
XX
DT 08-OCT-2002 (first entry)
XX
DE Human sbg10220MCTb protein.
XX
KW Human; secreted protein; immunosuppressive; cytostatic; nootropic;
KW neuroprotective; antitumour; vulnereary; antimicrobial; ophthalmological;
KW antiapikinsorian; antirheumatic; antithrombotic; dermatological;
KW hypotensive; cerebroprotective; vinucide; antiinflammatory; diabetes;
KW malignant tumour; hypertension; hypotension; obesity; bulimia; anorexia;
KW asthma; manic depression; dementia; delirium; mental retardation;
KW Huntington's disease; Tourette's syndrome; schizophrenia;
KW mental disorder; sexual development disorder; blood cascade dysfunction;
KW stroke; growth disorder.
XX
OS Homo sapiens.
XX
PN WO200222802-A1.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028462.
XX
PR 13-SEP-2000; 2000US-0232455P.
XX
PR 13-SEP-2000; 2000US-0232463P.
XX
PR 02-OCT-2000; 2000US-0237293P.
XX
PR 07-NOV-2000; 2000US-0246269P.
XX
PR 20-NOV-2000; 2000US-0252049P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
PI Agargwal P, Gogswell JP, Lai Y, Martensen SA, Smith RF, Strum JC,
PI Xie Q;
DR WPT; 2002-393963/42.
DR N-PSDB; ABL57732.
XX
XX Novel isolated secreted polypeptides and polynucleotides encoding them
XX useful for treating cancer, Alzheimer's disease, tumor metastasis,
XX autosomal recessive atypical hemolytic uremic syndrome, wound healing
XX disorder.
XX
XX 1; Page216-217; 246pp; English.

The invention relates to a novel isolated polypeptide (ABB80569-ABB806122) (secreted polypeptide) which is encoded by any one of 44 polynucleotide sequences (ABL57705-ABL57748) given in the specification. The polypeptides have immunosuppressive, cytostatic, nootropic, neuroprotective, antitumour, vulnerary, antithrombotic, ophthalmological, antiapikinsorian, antirheumatic, antidiabetic, metabolic, hypotensive, cerebroprotective, vinucide, and antiinflammatory activity. The polynucleotide and polypeptide are useful for treating diabetes, malignant tumours, hyper- and hypotension, obesity, bulimia, anorexia, asthma, manic depression, dementia, delirium, mental retardation, Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke

Sequence 458 AA:

Db	2	MARTEPDOCGMWVVLVSAFPOSALVFGVLRGCVFVEFVAFAFEQARVWMSIGI	61
Qy	61	AVDQFSGPVGSGALSTKRGPPRVMTGIIILAALGMLASFAFSLTHLYLSIGLSSGSMAL	120
Db	62	AVDQFSGPVGSGALSTKRGPPRVMTGIIILAALGMLASFAFSLTHLYLSIGLSSGSMAL	121
Qy	121	TEAPTLACSCYFSRRRLATGALTGVGLSSTFAPFQWLLSHYAWRGSLLVLSALSL	180
Db	122	TEAPTLACSCYFSRRRLATGALTGVGLSSTFAPFQWLLSHYAWRGSLLVLSALSL	181
Qy	181	HLVACGALLRPESLADPPAVGGRPAQLTSLHHGPEFLRTVVALTLNTNGYFIEYLLVAAH	240
Db	182	HLVACGALLRPESLADPPAVGGRPAQLTSLHHGPEFLRTVVALTLNTNGYFIEYLLVAAH	241
Qy	241	LQDLDMDPLPAEFLLSVVAISDIVERVSGWLGDAVPGVTRLMLMTLLTGVSALFPV	300
Db	242	LQDLDMDPLPAEFLLSVVAISDIVERVSGWLGDAVPGVTRLMLMTLLTGVSALFPV	301
Qy	301	AQAPTLVALLVAVYGTSGALAPLASVPELIGTRITICGGLLOMISIGLLGPPLS	360
Db	302	AQAPTLVALLVAVYGTSGALAPLASVPELIGTRITICGGLLOMISIGLLGPPLS	361
Qy	361	GYLRDVSNGVYTSFVAVAGAFILSGSGLLTLPHPFCSFTTSGPDLVTEALDTKPLPK	420
Db	362	GYLRDVSNGVYTSFVAVAGAFILSGSGLLTLPHPFCSFTTSGPDLVTEALDTKPLPK	421
Qy	421	EGLEGGLNSTESGPESQSITAPGQLLPRIGLHRTVP	457
Db	422	EGLEGGLNSTESGPESQSITAPGQLLPRIGLHRTVP	458
RESULT 4			
ABP61019			
ID	ABP61019	standard; protein; 426 AA.	
XX	XX	ABP61019;	
AC	XX		
XX	XX		
DT	10-SEP-2002	(first entry)	
XX	XX		
DE	XX	Novel human protein. SEQ ID 110.	
XX	XX		
KW	Human; cytosolic; vulnereary; antiarteriosclerotic; antiparkinsonian;		
KW	neotropic; neuroprotective; immunosuppressive; haemostatic;		
KW	antiinflammatory; cardiant; antitumor; virucide; antithyroid;		
KW	cerobroprotective; anorectic; metabolic; vaccine; cancer; infection;		
KW	wound healing disorders; atherosclerosis; Parkinson's disease;		
KW	Alzheimer's disease; autoimmune disorder; haematopoietic disorder;		
KW	inflammation; neoplastic disease; nervous system disorder;		
KW	cardiovascular disorders; pancreatitis; respiratory disorder;		
KW	hyperproliferation; systemic autoimmune disease; hyper-immunity;		
KW	developmental abnormality; gastrointestinal ulceration; neuropathy;		
KW	haematological disease; metabolic disease; sperm dysfunction;		
KW	thyroid disorder; hypothyroidism; brain damage; colitis;		
KW	cone photo- transduction deficiency; neurological disease; stroke;		
KW	angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;		
KW	trachea; thymus; lymph node; muscular system; obesity; anorexia;		
KW	growth abnormality; precocious puberty.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO200250105-A1.		
XX	XX		
PD	27-JUN-2002.		
XX	XX		
PF	17-DEC-2001; 2001WO-US049232.		
XX	XX		
PR	19-DEC-2000; 2000US-0256710P.		
PR	20-DEC-2000; 2000US-0257048P.		
PR	09-JAN-2001; 2001US-0260482P.		
PR	30-JAN-2001; 2001US-0264922P.		
PR	06-FEB-2001; 2001US-0266797P.		
PR	19-MAR-2001; 2001US-0276989P.		
PR	04-APR-2001; 2001US-0281515P.		

PR 08-MAY-2001; 2001US-0289622P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
PI Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;
PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
XX WPI: 2002-508784/54.
DR N-PSDB; ABO86184.
PT Secreted proteins and polynucleotides useful as vaccines for preventing
PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
PS Claim 1(a); Page 331-332; 335pp; English.
XX
XX The invention relates to an isolated polypeptide with signal sequences
CC which allow it to be secreted extracellularly or membrane associated. The
CC activity of polypeptides of the invention may be described as,
CC cyclostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC cardiant, antitumor, vitruclide, antithyroid, cerebroprotective, anorectic,
CC and metabolic. Polypeptides and polynucleotides of the invention are
CC useful in the treatment, or as a vaccine in the prevention of, cancer,
CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC inflammation, neoplastic diseases, nervous system related disorders and
CC cardiovascular disorders, pancreatitis, respiratory disorder,
CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC developmental abnormality, gastrointestinal ulceration, neuropathy,
CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC transduction deficiency, neurological diseases, stroke, angiodenesis,
CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC growth abnormalities, and alleviation of precocious puberty. The
CC sequences given in records ABP60965-ABP61019 represent novel human
CC proteins of the invention
CC
XX
XX Sequence 426 AA;
SQ
Query Match 92.4%; Score 2154; DB 5; Length 426;
Best Local Similarity 99.8%; Pred. No. 2,6e-189;
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 MARRTPEPPDGGRVYVLSAFPOSALVFGLRSFGVFEFVFAAFPEOARVSWIASIGI 60
DB 1 MARKREPPDGGWVWVLSAFPOSALVFGLRSFGVFEFVFAAFPEOARVSWIASIGI 60
OY 61 AVQFGSPVGSALSTKFGPRPVMTGCIILAIGMLIASPSTVLTLYLSIGLLSGGWL 120
DB 61 AVQFGSPVGSALSTKFGPRPVMTGCIILAIGMLIASPSTVLTLYLSIGLLSGGWL 120
OY 121 TPAFTLACISCFPSRRRSIATGALTGVGLSSFTFPAFFQWMLSHYAMGSLIVASLT 180
DB 121 TPAFTLACISCFPSRRRSIATGALTGVGLSSFTFPAFFQWMLSHYAMGSLIVASLT 180
OY 181 HLVACGALLRPSLAEDPAVGGPRAQUTSLHHGPFRLVTAALTINTGYFIPYHLVNA 240
DB 181 HLVACGALLRPSLAEDPAVGGPRAQUTSLHHGPFRLVTAALTINTGYFIPYHLVNA 240
OY 241 LODLMDPPLPAFLISVVAISDLVGRVVGWLGDAVPGVTLMLMTLTVGSIALPFV 300
DB 241 LODLMDPPLPAFLISVVAISDLVGRVVGWLGDAVPGVTLMLMTLTVGSIALPFV 300
OY 301 AQPAPLVALAVAGFTSGALAPLAFSVLPBILGTRRIYCGLLQMTESIGLLGPPLS 360
DB 301 AQPAPLVALAVAGFTSGALAPLAFSVLPBILGTRRIYCGLLQMTESIGLLGPPLS 360
OY 361 GYLKRVSGNYTASFVAGAFLLSGGILLTLPHFFCFSTTSGPQDLVTEALDTKVP LPK 420
DB 361 GYLKRVSGNYTASFVAGAFLLSGGILLTLPHFFCFSTTSGPQDLVTEALDTKVP LPK 420

DB 361 GYLKRVSGNYTASFVAGAFLLSGGILLTLPHFFCFSTTSGPQDLVTEALDTKVP LPK 420
OY 421 EGLE 424
DB 421 EGLE 424
RESULT 5
ID AAE16779
AAE16779 standard; protein; 426 AA.
XX
XX AAE16779;
XX
XX 09-APR-2002 (first entry)
XX
DE Human transporter and ion channel-16 (TRICH-16) protein.
XX
XX Human: transporter and ion channel-16; TRICH-16; neuroprotective; asthma;
XX noctropic; cyrostatic; cardiovascular; immunosuppressive; cardiomyopathy;
XX antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
XX Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
XX amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS;
XX Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
XX cell proliferative disorder; psoriasis; cardiac disease; hypertension;
XX bradyarrhythmia; gene expression; drug screening.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH 82..109
XX Domain /label= Transmembrane_domain
XX FT 338..356
XX FT /label= Transmembrane_domain
XX
XX MO200192304-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US017065.
XX
XX 26-MAY-2000; 2000US-0208424P.
XX PR 01-JUN-2000; 2000US-0209001P.
XX PR 08-JUN-2000; 2000US-0210588P.
XX PR 16-JUN-2000; 2000US-0212335P.
XX PR 22-JUN-2000; 2000US-0213747P.
XX PR 29-JUN-2000; 2000US-0215391P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Thornton M, Wajia NK, Yue H, Nguyen DB, Lai P, Gandhi AR;
XX Tribouley CM, Yao MG, Ramkumar J, Au-Yang J, Lu Y, Tang YT;
XX Azmouzi Y, Bruns CM, Griffin JA, Yang J, Sanjanwala MS, Raumann BE;
XX Lee EA, Hatalia A, Baughn WR, Green BD, Khan FA, Kearney L;
XX Elliot VS, Seilhamer JJ, Policky JL, Borowsky ML, Burford N, Ding L;
XX Lu DAM, Hillman JL;
XX
XX WPI: 2002-122055/16.
XX N-PSDB; AAD27269.
XX
XX New human transporters and ion channels (TRICH) polypeptides useful for
XX diagnosing, treating or preventing disorders associated with aberrant
XX expression of TRICH.
XX
XX
XX Claim 1; Page 166; 210pp; English.
XX
XX The invention relates to human transporters and ion channels (TRICH)
XX polypeptides and their cDNA molecules. The nucleic acid and polypeptide
XX sequences are useful in the diagnosis, treatment, and prevention of
XX disorders associated with transport (akinesia, cystic fibrosis, Bell's
XX palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
XX amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's
XX muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
XX asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);

CC cardiac disease (angina, hypertension, or bradyarrhythmia) and in the
CC assessment of the effects of exogenous compounds on the expression of
CC nucleic acid and amino acid sequences of transporters and ion channels.
CC The polynucleotides may be used to detect and quantify gene expression in
CC biopsied tissues in which TRIC expression may be correlated with a
CC disease, to generate hybridization probes for mapping naturally occurring
CC genomic sequence, and in drug screening. The present sequence is human
CC TRIC-16 protein

Sequence 426 AA;

Query March	92.3%	Score 2151	DB 5	Length 426
Best Local Similarity	99.5%	Pred. No. 4.9e-189		
Matches 422	Conservative	1	Mismatches	0

QY	1	IMARTPEPDGGMWRVVVLSAF	FOSALVFGVLR	EEGVFE	PAFAPEQAA	RVSWIASIGI	60
Db	1	NARRTERPDGGMWVVVLSAF	FOSALVFGVLR	EEGVFE	PAFAPEQAA	RVSWIASIGI	60
QY	61	AVOQFSPVGSALSTKFGPR	PVMTGGII	LAALGMLAS	FATSLTH	YUSIGLSSGNAL	12
Db	61	AVOQFSPVGSALSTKFGPR	PVMTGGII	LAALGMLAS	FATSLTH	YUSIGLSSGNAL	12
QY	121	TEAPTLACLSCTFESRRSLAT	GLALTVGLSSFTTAP	PEOWMLSH	YARGSILLYASATL		18
Db	121	TEAPTLACLSCTFESRRSLAT	GLALTVGLSSFTTAP	PEOWMLSH	YARGSILLYASATL		18
QY	181	HLVACGALLRPSSLAEDPA	VGGPRQOLTS	LSLHGGP	LRYVALTLINTGYE	PYLHLVAH	24
Db	181	HUVACGALLRPSSLAEDPA	VGGPRQOLTS	LSLHGGP	LRYVALTLINTGYE	PYLHLVAH	24
QY	241	LODLWDMDPLPAAFLLSV	VAISDLVGRVVS	GMVGDV	PGPVRRLMLMTL	TGVSALFPV	30
Db	241	LODLWDMDPLPAAFLLSV	VAISDLVGRVVS	GMVGDV	PGPVRRLMLMTL	TGVSALFPV	30
QY	301	AOAPPLVALVALVAVGFTS	GALAPLAFSVLP	PELICTRRI	YCGILGLQMI	IESIGLGPPLS	36
Db	301	AOAPPLVALVALVAVGFTS	GALAPLAFSVLP	PELICTRRI	YCGILGLQMI	IESIGLGPPLS	36
QY	361	CYIADVSGNVAASFVAGAF	LLSSGILLTPH	FFCSTSTT	SGPQDLVT	BALDTKVP	42
Db	361	CYIADVSGNVAASFVAGAF	LLSSGILLTPH	FFCSTSTT	SGPQDLVT	BALDTKVP	42
QY	421	EGLE	424				
Db	421	EGLE	424				

ESULT 6
ABG32785
ABG32785 standard; protein; 426 AA.

Human monocarboxylic acid transporter protein TCH081 protein.

Human; hepatotropic; antidiabetic; nephrotoxic; immunosuppressant; antinflammatory; antiallergic; cytotoxic; antiviral; vasotropic; neuroproliferative; nootropic; liver disease; diabetes; kidney disease; metabolic acidosis; muscular disease; spleen disease; immunodeficiency; autoimmune disease; inflammatory disease; allergy; genital disease; digestive disease; central nervous system disorder; circulatory disease; cancer; monocarboxylic acid transporter protein TCH081.

Homo sapiens.
WO200262998-A1
15-AUG-2002.

PF 05-FEB-2002; 2002WO-JP000914.
XX
PR 06-FEB-2001; 2001JP-00030172.
PR 21-JUN-2001; 2001JP-00188708.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI
XX
PI Nakanishi A, Sagiya Y;
XX
DR WPI, 2002-627556/67.
N-PSDB; ABSS3751.
XX

PT for screening compounds modifying its activity which can be used as drugs.

Claim 1; Page 82-84; 102pp; Japanese

monocarboxylic acid transporter protein TGH081 and its salts. The protein of the invention may have hepatotropic, antifibrotic, nephrotropic, immunostimulant, immunosuppressant, antiinflammatory, antiallergic, cytostatic, anticancer, vasotrophic, neuroprotective and nontropic activity. Modification of transport of monocarboxylic acids and amino acids into cells mediated by the TGH081 protein. The protein of the invention is useful for the treatment, prevention and diagnosis of a wide range of disorders including liver disease, diabetes, kidney disease, metabolic acidosis, muscular liver disease, spleen disease, immunodeficiency, autoimmune diseases, inflammatory diseases, allergies, genital diseases, digestive diseases, diseases of the central nervous system, circulatory diseases and cancer. The present sequence represents the human monocarboxylic acid transporter protein TGH081 of the invention

Sequence 426 AA

Query Match	92.3%	Score 2151;	DB 5;	Length 426;
Best Local Similarity	99.5%;	Pred. No. 4.9e-169;		
Matches 422; Conservative	1;	Mismatches 1;		

[illegible]

RESULT

VD16770
CD AD16770 standard; protein; 426 AA.
XX
VC AD16770;
XX
XX 15-APR-2004 (first entry)
XX
XX Human NOVX protein to treat human pathological conditions SeqID306.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cyostatic; cardiatic; antiinflammatory; immunosuppressive; antiallergic;
XX hemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
XX antiasthmatic; nephrotoxic; antiarthritic; hepatotoxic;
XX neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
XX relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
XX chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
XX
XX WO200268649-A2.
XX
XX 06-SEP-2002.
XX
XX 31-JAN-2002; 2002WO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282992P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296646P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312904P.

PR 21-AUG-2001; 2001US-0313902P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316477P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernev VT, Spytek KA, Zerhusen BD, Patumrajan M, Shinkets RA;
XX Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
XX Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
XX Putak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
XX WPI; 2002-706998/76.
XX
XX N-PSDB; AD16769.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX
XX Claim 1; SEQ ID NO 306; 149bp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
XX thereof, which have properties related to the stimulation of biochemical
XX or physiological responses in a cell, tissue, organ or organism.
XX Specifically, it refers to the use of biologically active fragments for
XX diagnostic and prognostic assays and furthermore in the treatment of
XX diverse pathological conditions. The present invention describes novel
XX human and murine NOVX proteins, as well as methods to modulate their
XX expression using antisense oligos, ribozymes and peptide nucleic acids.
XX The NOVX polypeptides, polynucleotides and antibodies are useful in
XX treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
XX atherosclerosis, cancer and diabetes. Furthermore, they may be used in
XX treating or preventing diseases such as inflammation, autoimmune
XX disorders, allergies, blood disorders, acquired immunodeficiency syndrome
XX (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
XX arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
XX and epilepsy. Accordingly, these molecules have many activities including
XX cyostatic, cardiatic, antiinflammatory, immunosuppressive, antiallergic,
XX haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
XX antiasthmatic, nephrotoxic, antiarthritic, hepatotoxic,
XX neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
XX relaxant and anticonvulsant. In addition, they are useful in screening
XX assays to identify small molecules that modulate or inhibit, for example,
XX neurogenesis, wound healing and angiogenesis. The nucleic acids are also
XX used as in chromosome mapping, tissue typing, preventive medicine and
XX pharmacogenomics. This polypeptide is a human NOVX protein of the
XX invention.
XX
XX Sequence 426 AA;
SQ
Query Match 92.2%; Score 2150; DB 5; Length 426;
Best Local Similarity 99.5%; Pred. No. 6e-189;
Matches 422; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MARTEPPDGGKGVVLSAFPOGALVGVLRSGVFVFVFAAFEOARVSIASIGI 60
Db 1 MARTEPPDGGKGVVLSAFPOGALVGVLRSGVFVFVFAAFEOARVSIASIGI 60
QY 61 AVQFGSPVGSALSTKCGPPVVTGILALGMLASPATSLTHLVLISGLSGGMAI 120
Db 61 AVQFGSPVGSALSTKCGPPVVTGILALGMLASPATSLTHLVLISGLSGGMAI 120
QY 121 TFAPTLACSCYFRRRLATGLALTGVGLSFFFAFPQWLISHVMRGSLLVSL 180
Db 121 TFAPTLACSCYFRRRLATGLALTGVGLSFFFAFPQWLISHVMRGSLLVSL 180
121 TFAPTLACSCYFRRRLATGLALTGVGLSFFFAFPQWLISHVMRGSLLVSL 180

QY 181 HLVAAGALLRPPSLAEDPAVGPPRAQLTSLHHGPFLEHYVALTLINTGYFIPYLIHVAH 240
 DB 181 HLVAAGALLRPPSLAEDPAVGPPRAQLTSLHHGPFLEHYVALTLINTGYFIPYLIHVAH 240
 QY 241 LODIDMDPLPAAPFLISVVAISDLVGRVVSGLGDAVPGPVRTLMMLTTLTGVSALFPV 300
 DB 241 LODIDMDPLPAAPFLISVVAISDLVGRVVSGLGDAVPGPVRTLMMLTTLTGVSALFPV 300
 QY 301 AOAFTALVALAVAGFTSGALAPLAFSVLPFLIGTRIRYCGLLQMTESIGLGPPLS 360
 DB 301 AOAFTALVALAVAGFTSGALAPLAFSVLPFLIGTRIRYCGLLQMTESIGLGPPLS 360
 QY 361 GYLKDVSGNVTASVVAAGAFLLSSGILLTLPHFFCSTTTSGPDVTEALDTKVP LPK 420
 DB 361 GYLKDVSGNVTASVVAAGAFLLSSGILLTLPHFFCSTTTSGPDVTEALDTKVP LPK 420
 QY 421 EGLE 424
 DB 421 EGLE 424

RESULT 8
 AEG13486
 ID AEG13486 standard; protein; 426 AA.
 AC AEG13486;
 XX
 DT 20-APR-2006 (first entry)
 XX
 DE Amino acid sequence for human NOV6c.
 XX
 KW NOV polypeptide; substrate; screening; obesity; diabetes;
 KW myocardial disease; atherosclerosis; hypertension; scleroderma;
 KW prostate tumor; acquired immune deficiency syndrome; asthma;
 KW multiple sclerosis; infectious disease; anorexia nervosa;
 KW Alzheimer's disease; parkinson's disease; anorectic; antidiabetic;
 KW cardiac; cardiovascular; gen.; antiarteriosclerotic; hypotensive;
 KW dermatological; cytoskeletal; anti-hiv; antiasclerotic; neuroprotective;
 KW antimicrobial; anabolic; eating-disorders-gen.; nootropic;
 KW antiparkinsonian.
 XX
 OS Homo sapiens.
 XX
 PN WO2006020326-A2.
 XX
 PD 23-FEB-2006.
 XX
 PF 20-JUL-2005; 2005WO-US025762.
 XX
 PR 13-AUG-2004; 2004US-0601306P.
 PR 19-JUL-2005; 50US-08876322.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Berghs C, Catterton E, Chaudhuri A, Ellerman KE, Ort TA;
 DR WPI; 2006-184398/19.
 DR N-PDB; AEG13485.
 XX
 PT Identifying compounds that modulate target polypeptide activity, by
 PT combining test compound with target polypeptide and substrate of the
 PT target polypeptide, and determining if the compound modulates activity of
 PT the target polypeptide.
 XX
 PS Claim 1; SEQ ID NO 30; 181bp; English.
 XX
 CC The invention relates to a method of identifying compounds that modulate
 CC target polypeptide activity. The method comprises: (a) combining a test
 CC compound with a target polypeptide and a substrate of the target
 CC polypeptide; and (b) determining whether the test compound modulates the
 CC activity of the target polypeptide, where the target polypeptide
 CC comprises an amino acid sequence selected from SEQ ID NO. 2n, where n is
 CC 1-16, the amino acid sequence that is at least 95 % identical to SEQ ID

CC NO. 2n, the amino acid sequence of at least one domain of SEQ ID NO. 2n,
 CC or the amino acid sequence that is at least 95 % identical to the at
 CC least one domain of SEQ ID NO. 2n. Also described are: (1) an antibody
 CC that immunospecifically binds to the target polypeptide; (2) a method of
 CC identifying a potential therapeutic agent for use in treatment of a
 CC pathology, where the pathology is related to aberrant expression or
 CC aberrant physiological interactions of a target polypeptide; (3)
 CC screening for a modulator of activity or of latency or predisposition to
 CC pathology associated with a target polypeptide; and (4) a nucleic acid
 CC sequence encoding a target polypeptide of the invention, where the
 CC nucleic acid comprises a sequence selected from SEQ ID NO. 2n-1. The
 CC method of the invention is useful for identifying compounds that modulate
 CC target polypeptide activity. The compounds can be used for the treatment
 CC of obesity or diabetes. It can also be used for treating pathology
 CC related to aberrant expression or aberrant physiological interactions of
 CC a target polypeptide. Pathologies include cardiomyopathy,
 CC atherosclerosis, hypertension, scleroderma, prostate cancer, AIDS,
 CC bronchial asthma, multiple sclerosis, infectious disease, anorexia,
 CC Alzheimer's disease, or Parkinson's disease. This sequence represents a
 CC human NOV protein.
 XX
 SQ Sequence 426 AA;
 XX
 QY Query Match 92.2%; Score 2150; DB 10; Length 426;
 DB Best Local Similarity 99.5%; Pred. No. 66-109;
 DB Matches 422; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MARTEPPDGGWGRVVLISAFQOSALVFCVLRSPGVFVFVFAAEBOARVSWIASIGI 60
 DB 1 MARTEPPDGGWGRVVLISAFQOSALVFCVLRSPGVFVFVFAAEBOARVSWIASIGI 60
 QY 61 AVOQGSVPYGSALSTKCPGRRPVMTGGILALGMLASPATSLTHLYSTIGLSGGMAL 120
 DB 61 AVOQGSVPYGSALSTKCPGRRPVMTGGILALGMLASPATSLTHLYSTIGLSGGMAL 120
 QY 121 TPAPLACISCFPSRRSLATGALTGVLSTFTPAFPFOWMLSHYMRGSLIVASLSL 180
 DB 121 TPAPLACISCFPSRRSLATGALTGVLSTFTPAFPFOWMLSHYMRGSLIVASLSL 180
 QY 181 HLVAAGALLRPPSLAEDPAVGPPRAQLTSLHHGPFLEHYVALTLINTGYFIPYLIHVAH 240
 DB 181 HLVAAGALLRPPSLAEDPAVGPPRAQLTSLHHGPFLEHYVALTLINTGYFIPYLIHVAH 240
 QY 241 LODIDMDPLPAAPFLISVVAISDLVGRVVSGLGDAVPGPVRTLMMLTTLTGVSALFPV 300
 DB 241 LODIDMDPLPAAPFLISVVAISDLVGRVVSGLGDAVPGPVRTLMMLTTLTGVSALFPV 300
 QY 301 AOAFTALVALAVAGFTSGALAPLAFSVLPFLIGTRIRYCGLLQMTESIGLGPPLS 360
 DB 301 AOAFTALVALAVAGFTSGALAPLAFSVLPFLIGTRIRYCGLLQMTESIGLGPPLS 360
 QY 361 GYLKDVSGNVTASVVAAGAFLLSSGILLTLPHFFCSTTTSGPDVTEALDTKVP LPK 420
 DB 361 GYLKDVSGNVTASVVAAGAFLLSSGILLTLPHFFCSTTTSGPDVTEALDTKVP LPK 420
 QY 421 EGLE 424
 DB 421 EGLE 424

RESULT 9
 ADN42424
 ID ADN42424 standard; protein; 426 AA.
 XX
 AC ADN42424;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human novel protein NOV 96c.
 XX
 KW Human; NOV; cancer; diabetes; cardiomyopathy; atherosclerosis.
 XX
 OS Homo sapiens.

XX US2004033493-A1.
 2D 19-FEB-2004.
 XX 31-JAN-2002; 2002US-00072012.
 XX 31-JAN-2001; 2001US-0265395P.
 PR 31-JAN-2001; 2001US-0265412P.
 PR 31-JAN-2001; 2001US-0265514P.
 PR 31-JAN-2001; 2001US-0265517P.
 PR 02-FEB-2001; 2001US-0266406P.
 PR 05-FEB-2001; 2001US-0266767P.
 PR 07-FEB-2001; 2001US-0266975P.
 PR 08-FEB-2001; 2001US-0267459P.
 PR 09-FEB-2001; 2001US-0267823P.
 PR 15-FEB-2001; 2001US-0268974P.
 PR 26-FEB-2001; 2001US-0271664P.
 PR 27-FEB-2001; 2001US-0271855P.
 PR 02-MAR-2001; 2001US-0272788P.
 PR 02-MAR-2001; 2001US-0273046P.
 PR 14-MAR-2001; 2001US-0275925P.
 PR 14-MAR-2001; 2001US-0275947P.
 PR 14-MAR-2001; 2001US-0275950P.
 PR 15-MAR-2001; 2001US-0275989P.
 PR 15-MAR-2001; 2001US-0276448P.
 PR 16-MAR-2001; 2001US-0276397P.
 PR 16-MAR-2001; 2001US-0276768P.
 PR 20-MAR-2001; 2001US-0278652P.
 PR 26-MAR-2001; 2001US-0278775P.
 PR 26-MAR-2001; 2001US-0278778P.
 PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282992P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313930P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 XX
 XX (TCHE/) TCHEVNE V T.
 PA (SPYT/) SPYTER K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PATR/) PATTURAJAN M.
 PA (SHIM/) SHIMKETS R A.
 PA (LIL/) LI L.
 PA (GANG/) GANGCOLLI E A.
 PA (PADI/) PADIGARU M.
 PA (ANDE/) ANDERSON D W.
 PA (RAST/) RASTELLI L.
 PA (MILL/) MILLER C E.

PA (GERL/) GERLACH V.
 PA (TAUP/) TAUPIER R J.
 PA (GUSE/) GUSEV V Y.
 PA (COLM/) COLMAN S D.
 PA (WOLE/) WOLENC A R.
 PA (PENA/) PENA C E A.
 PA (FORT/) FURTAK K.
 PA (GROS/) GROSSE W M.
 PA (ALSO/) ALSOBROOK J P.
 PA (LEPL/) LEPLEY D M.
 PA (RIEG/) RIEGER D K.
 PA (BURG/) BURGESS C E.
 XX
 XX Tchervne VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;
 PI Li L, Gangcoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
 PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
 PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX
 XX WPI; 2004-180039/17.
 DR N-PSDB; ADN42423.
 DR
 XX
 XX Isolated NOVX polypeptides and polynucleotides, useful for preventing
 PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
 PT atherosclerosis.
 PT
 XX
 XX Claim 1; SEQ ID NO 306; 1309pp; English.
 XX
 XX The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
 CC including splice variants) and the nucleic acids (NA) that encode them.
 CC Also included are the mature NOVX proteins (and their encoding
 CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
 CC vector, an antibody that binds immunospecifically to NOVX, determining
 CC the presence or amount of NOVX in a sample, determining the presence or
 CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,
 CC modulating the activity of NOVX, treating or preventing a NOVX-associated
 CC disorder determining the presence of or predisposition to a disease
 CC associated with altered levels of NOVX and treating a pathological state
 CC in a mammal comprising administering a polypeptide which is at least 95%
 CC identical to NOVX (or fragment). NOVX and NA may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
 CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
 CC antagonists may also be used to down regulate expression and activity of
 CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
 CC detecting the presence of NOVX in samples (e.g. by enzyme linked
 CC immunosorbant assay (ELISA). The agents and methods may be used in this
 CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
 CC and/or atherosclerosis. The present sequence represents a NOVX protein.
 XX
 XX Sequence 426 AA:
 Query Match 91.9%; Score 2143; DB 8; Length 426;
 Best Local Similarity 99.3%; Pred. No. 2,7e-188;
 Matches 421; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MARTEPPDGMGVVVLSAFPOSALVGVLRSGVFVEFVAAFEOARVSIATIGI 60
 DB 1 MARTEPPDGMGVVVLSAFPOSALVGVLRSGVFVEFVAAFEOARVSIATIGI 60
 QY 61 AVQFGSPVGSALSTKFPKPPVVTGIIALGMLASFATSLTHLYLSIGLSSGSMAL 120
 DB 61 AVQFGSPVGSALSTKFPKPPVVTGIIALGMLASFATSLTHLYLSIGLSSGSMAL 120
 QY 121 TEAPTLACISCFYSRRSLATGALTGVGSSFTFAFPOMLSHYVMRGSILVSLSL 180
 DB 121 TEAPTLACISCFYSRRSLATGALTGVGSSFTFAFPOMLSHYVMRGSILVSLSL 180
 QY 181 HLVACGALLRPPSLAEDPAVGGPRAQLTSLHHGPFRLRYVAULTLINTGYFIPYHLVAH 240
 DB 181 HLVACGALLRPPSLAEDPAVGGPRAQLTSLHHGPFRLRYVAULTLINTGYFIPYHLVAH 240
 QY 241 LQDDMDPLPAAFLLVVAISDLVGRVVGMLGDAVGPPTRLMLMTTTLTGVSALFVPV 300

Db 241 LQDLMDPLPAFLSLVVAISDLVGRVVSGLGDAVPGCVTRLMLMWTLLTGVSLALPVPV 300
QY 301 AQAAPALVALAVAGFTSGALAPLAFSVLPBELLIGTRRIYCGILQMIESTIGLIGPLPS 360
Db 301 AQAAPALVALAVAGFTSGALAPLAFSVLPBELLIGTRRIYCGILQMIESTIGLIGPLPS 360
QY 361 GYLDPVSGNNTYASRFVACAFILSGGILLTLPHFPCFSTTTSGPDLVTEALDTKVPPLPK 420
Db 361 GYLDPVSGNNTYASRFVACAFILSGGILLTLPHFPCFSTTTSGPDLVTEALDTKVPPLPK 420
QY 421 EGLE 424
Db 421 EGLE 424

RESULT 10
ID AD116802 standard; protein, 427 AA.
AC AD116802;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein homologue Segid 338.
XX
KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
XX
OS Homo sapiens.
XX
PN WO200266649-A2;
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002WO-US002785.
XX
PR 31-JAN-2001; 2001US-0263395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 02-FEB-2001; 2001US-0265517P.
PR 05-FEB-2001; 2001US-0266406P.
PR 07-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 08-FEB-2001; 2001US-0267057P.
PR 09-FEB-2001; 2001US-0267459P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 02-MAR-2001; 2001US-0271855P.
PR 14-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278755P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0283992P.
PR 11-APR-2001; 2001US-0283983P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.

PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 13-JUN-2001; 2001US-0299324P.
PR 16-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 21-AUG-2001; 2001US-0313908P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323179P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.
XX
PA Tchernev VT, Spyrek KA, Zerhusen BD, Patuturajan M, Shinkets RA;
XX Li L, Gangolli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
PI Furrak K, Grose WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2002-706998/76.
XX
PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Disclosure: SEQ ID NO 338; 1498bp; English.
XX

This invention relates to a novel nucleic acids, and encoded polypeptides or thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy, CC and epilepsy. Accordingly, these molecules have many activities including CC cytostatic, cardiac antiinflammatory, immunosuppressive, antiallergic, CC haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic, CC antiaesthetic, nephrotoxic, antiautistic, hepatotropic, CC neuroprotective, neurotropic, antibacterial, vinocide, antiparasitic, CC relaxant and anticonvulsant. In addition, they are useful in screening CC assays to identify small molecules that modulate or inhibit, for example, CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also CC used as in chromosome mapping, tissue typing, preventive medicine and CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein of the invention.

Seq Sequence 427 AA;

Query Match 91.9%; Score 2142.5; DB 5; Length 427;
Best Local Similarity 99.3%; Pred. No. 3e-188;
Matches 422; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 MARRTEPPDGGWG-RVVVLSAFPOSALVFGVLSFGVFEEFVVAFAFEQARVSWIASIG 59
Db 1 MARRTEPPDGGWGVVVLSAFQSAIVFGVLSFGVFEEFVVAFAFEQARVSWIASIG 60

CC	14-MAR-2001;	2001US-0275989P.
PR	15-MAR-2001;	2001US-0276448P.
PR	15-MAR-2001;	2001US-0276450P.
PR	16-MAR-2001;	2001US-0276397P.
PR	16-MAR-2001;	2001US-0276768P.
PR	20-MAR-2001;	2001US-0278652P.
PR	26-MAR-2001;	2001US-0278775P.
PR	26-MAR-2001;	2001US-0278778P.
PR	29-MAR-2001;	2001US-0279882P.
PR	29-MAR-2001;	2001US-0279884P.
PR	30-MAR-2001;	2001US-0280147P.
PR	11-APR-2001;	2001US-0282992P.
PR	11-APR-2001;	2001US-0283083P.
PR	20-APR-2001;	2001US-0285133P.
PR	23-APR-2001;	2001US-0285749P.
PR	03-MAY-2001;	2001US-0288327P.
PR	03-MAY-2001;	2001US-0288504P.
PR	29-MAY-2001;	2001US-02944047P.
PR	30-MAY-2001;	2001US-0294473P.
PR	08-JUN-2001;	2001US-0296964P.
PR	18-JUN-2001;	2001US-0298959P.
PR	19-JUN-2001;	2001US-0299324P.
PR	13-AUG-2001;	2001US-0312020P.
PR	16-AUG-2001;	2001US-0312889P.
PR	16-AUG-2001;	2001US-0312908P.
PR	21-AUG-2001;	2001US-0313390P.
PR	26-AUG-2001;	2001US-0315470P.
PR	31-AUG-2001;	2001US-0315447P.
PR	07-SEP-2001;	2001US-0318115P.
PR	07-SEP-2001;	2001US-0318118P.
PR	12-SEP-2001;	2001US-0318740P.
PR	19-SEP-2001;	2001US-0323379P.
PR	18-OCT-2001;	2001US-0330245P.
PR	18-OCT-2001;	2001US-0330308P.
PR	14-NOV-2001;	2001US-0332701P.
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Tchernenov VT, Spytek KA, Zerhusen BD, Paturajan M, Shimketa RA;	
PI	Li L, Gargoli EA, Padigan M, Anderson DW, Rastelli L, Miller CE;	
PI	Gi L, Gargoli EA, Tsapler RJ, Gusev VY, Colman SD, Wolenc AR,	
PI	Futak K, Grosse WM, Alsdbrook JP, Lepley DW, Rieger DK, Burgess CE,	
XX		
DR	WPI; 2002-706998/76.	
XX		
PT	New NOXV polypeptides and nucleic acids, useful for preventing or	
PT	treating NOXV-associated disorders, e.g. cancer, cardiomyopathy,	
PT	atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or	
PT	pharmacogenomics.	
XX		
XX		
XX	Disclosure; SEQ ID NO 779; 1498pp; English.	
CC	This invention relates to a novel nucleic acid, and encoded polypeptides	
CC	thereof, which have properties related to the stimulation of biochemical	
CC	or physiological responses in a cell, tissue, organ or organism.	
CC	Specifically, it refers to the use of biologically active fragments for	
CC	diagnostic and prophetic assays and furthermore in the treatment of	
CC	diverse pathological conditions. The present invention describes novel	
CC	human and murine NOXV proteins, as well as methods to modulate their	
CC	expression using antisense oligos, ribozymes and peptide nucleic acids.	
CC	The NOXV polypeptides, polynucleotides and antibodies are useful in	
CC	treating or preventing NOXV-associated disorders, e.g. cardiomyopathy	
CC	atherosclerosis, cancer and diabetes. Furthermore, they may be used in	
CC	treating or preventing diseases such as inflammation, autoimmune	
CC	disorders, allergies, blood disorders, acquired immunodeficiency syndrome	
CC	(AIDS), obesity, asthma, immunoglobulin (IgA) nephropathy, cirrhosis,	
CC	arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy	
CC	and epilepsy. Accordingly, these molecules have many activities including	
CC	cytostatic, cardiac, antitumor, immunosuppressive, antiallergic,	
CC	hemostatic, anti-HIV, antidiabetic, antianorectic, anorectic,	
CC	antiasmatic, nephrotropic, antirheptic, hepatotropic,	
CC	neuroprotective, nootropic, antibacterial, virucide, antiparasitic,	
CC	relaxant and anticonvulsant. In addition, they are useful in screening	

CC assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein of the invention.

XX Sequence 427 AA;

Query Match
Best Local Similarity 91.9%; Score 2142.5; DB 5; Length 427;
Matches 422; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MARTRPPDGGWG-RVVVLSAFQSAIVFGVLRFGVFVEFVAFAFEQARVSWIASIG 59
D 1 MARTRPPDGGWGKVVVLSAFQSAIVFGVLRFGVFVEFVAFAFEQARVSWIASIG 60
QY 60 IAVQGFQSPVGSALSTKFGPRPVMTGTLAALGMLASFATSLTHLYSLIGLSGSGMA 119
D 61 IAVQGFQSPVGSALSTKFGPRPVMTGTLAALGMLASFATSLTHLYSLIGLSGSGMA 120
QY 120 LTFAPTLACSCYFSRRSLATGLATGVGLSFTFAPFPQMLSHYAMGSLILVSALS 179
D 121 LTFAPTLACSCYFSRRSLATGLATGVGLSFTFAPFPQMLSHYAMGSLILVSALS 180
QY 180 LHTVACGALLRPPSLAEDPAVGGPRAQLTSLHGPRLRTVALTLINTGYFPIYHLVA 239
D 181 LHTVACGALLRPPSLAEDPAVGGPRAQLTSLHGPRLRTVALTLINTGYFPIYHLVA 240
QY 240 HLODLDMDLPAALFLISVAISDLVGRVVSGLMDAPGVPFRLMLMTLTVGSALP 299
D 241 HLODLDMDLPAALFLISVAISDLVGRVVSGLMDAPGVPFRLMLMTLTVGSALP 300
QY 300 VAQAPFALVAVAAGTSGALAPLAFSLPELIGTRIRYICGILQIMESIGLIGPL 359
D 301 VAQAPFALVAVAAGTSGALAPLAFSLPELIGTRIRYICGILQIMESIGLIGPL 360
QY 360 SGYLRDVSQNTYASRVVAGAFLLSGGILLTPHFPCSTTTSGQDLYTEALDKVPLP 419
D 361 SGYLRDVSQNTYASRVVAGAFLLSGGILLTPHFPCSTTTSGQDLYTEALDKVPLP 420
QY 420 KEGLE 424
D 421 KEGLE 425

RESULT 12
AD16766 standard; protein, 426 AA.

AD16766;
15-APR-2004 (first entry)

Human NOVX protein to treat human pathological conditions SeqID302.
human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
inflammation; autoimmune disorder; allergy; blood disorder;
acquired immunodeficiency syndrome; AIDS; obesity; asthma;
immunoglobulin (IgA) nephropathy; cirrhosis; arthritis;
Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
cytostatic; candida; antiinflammatory; immunosuppressive; antiallergic;
haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
antistatic; nephrotropic; anticholesteric; hepatotropic;
neuroprotective; nootropic; antibacterial; vitamin; antiparasitic;
relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
chromosome mapping; tissue typing; pharmacogenomic.

Homo sapiens.
MO20026649-A2.
06-SEP-2002.

PF 31-JAN-2002; 2002W0-US002785.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 08-FEB-2001; 2001US-0267057P.
PR 09-FEB-2001; 2001US-0267459P.
PR 15-FEB-2001; 2001US-0267823P.
PR 26-FEB-2001; 2001US-0268774P.
PR 27-FEB-2001; 2001US-0271664P.
PR 02-MAR-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 14-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
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PR 26-MAR-2001; 2001US-0278752P.
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PR 29-MAR-2001; 2001US-0279882P.
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PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
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PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
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PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
PA (CUBA-) CUBAGEN CORP.
XX
PI Tchernen VV, Spytek KA, Zernusen BD, Parturajan M, Shinkets RA,
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Kastelli L, Miller CE,
PI Gerlach VL, Taupier RJ, Gusev VY, Coleman SD, Wolenc AR, Pena CE,
PI Furtak K, Grosse WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
DR WPI, 2002-706998/76.
DR N-PBDB, AD16765.
XX
PI New NOVX polypeptides and nucleic acids, useful for preventing or
PI treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PI atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PI pharmacogenomics.
PS Claim 1; SEQ ID NO 302; 1498bp; English.

X This invention relates to a novel nucleic acids, and encoded polypeptides
C thereof, which have properties related to the stimulation of biochemical
C or physiological responses in a cell, tissue, organ or organism.
C Specifically, it refers to the use of biologically active fragments for
C diagnostic and prognostic assays and furthermore in the treatment of
C diverse pathological conditions. The present invention describes novel
C human and murine NOVX proteins, as well as methods to modulate their
C expression using antisense oligos, ribozymes and peptide nucleic acids.
C The NOVX polypeptides, polynucleotides and antibodies are useful in
C treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
C atherosclerosis, cancer and diabetes. Furthermore, they may be used in
C treating or preventing diseases such as inflammation, autoimmune
C disorders, allergies, blood disorders, acquired immunodeficiency syndrome,
C (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
C arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
C and epilepsy. Accordingly, these molecules have many activities including
C cytoskeletal, cardiant, anti-inflammatory, immunosuppressive, antiallergic,
C haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
C antiasthmatic, nephroprotective, antibacterial, virucide, antiparasitic,
C neuroprotective, nootropic, antidiabetic, antiparasitic, antiparasitic,
C relaxant and anticonvulsant. In addition, they are useful in screening
C assays to identify small molecules that modulate or inhibit, for example,
C neurogenesis, wound healing and angiogenesis. The nucleic acids are also
C used as in chromosome mapping, tissue typing, preventive medicine and
C pharmacogenomics. This polypeptide is a human NOVX protein of the
C invention.

XX Sequence 426 AA;

Query Match 91.9%; Score 2142; DB 5; Length 426;
Best Local Similarity 99.1%; Pred. No. 3.3e-188;
Matches 420; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2Y 1 MARTEPDGCGMGRVYVLSAFPOSALVFGVLRSGVFVEFEVVAFEEOAARVMTASIGI 60
2b 1 WARRTEPDGCGMGRVYVLSAFPOSALVFGVLRSGVFVEFEVVAFEEOAARVMTASIGI 60
2Y 61 AVOOTGSPVGSALSTKFGPRPVMTGILALGMLASFATSLTHLYLSIGLLSGSGMAL 120
2b 61 AVQCFGSPVGSALSTKFGPRPVMTGILALGMLASFATSLTHLYLSIGLLSGSGMAL 120
2Y 121 TPAFTLALSCYFSRRSLATGLATGVLSSTTAPFPOMLSHYANRGSLLVSASL 180
2b 121 TPAFTLALSCYFSRRSLATGLATGVLSSTTAPFPOMLSHYANRGSLLVSASL 180
2Y 181 HUVAAGALLRPPSLAEDPAVGGPRAQLTSLHGFLLRYVALTLINTGYFLPYLHLVAH 240
2b 181 HUVAAGALLRPPSLAEDPAVGGPRAQLTSLHGFLLRYVALTLINTGYFLPYLHLVAH 240
2Y 241 LODLDWDPPLPAAFLLISVAISDLVGRVVSVMGDVAPGPVTRLLMLMTTLTGVSIALFPV 300
2b 241 LODLDWDPPLPAAFLLISVAISDLVGRVVSVMGDVAPGPVTRLLMLMTTLTGVSIALFPV 300
2Y 301 AOAFTALVALAVAGFTSGALAPLAFSVLPFLIGRRIRYCGILQWESIGLLGPPLS 360
2b 301 AOAFTALVALAVAGFTSGALAPLAFSVLPFLIGRRIRYCGILQWESIGLLGPPLS 360
2Y 361 GYLKRVSGNYTASFVVAAGFLTSSGILLTLPHFFCFSTTTSGPDVLTALDTKVPPLPK 420
2b 361 GYLKRVSGNYTASFVVAAGFLTSSGILLTLPHFFCFSTTTSGPDVLTALDTKVPPLPK 420
2Y 421 EGLE 424
2b 421 EGLE 424

RESULT 13
AD116768
XX AD116768 standard; protein; 426 AA.
XX AD116768;
XX

DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein to treat human pathological conditions SegID304.
XX
KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW haemostatic; cardiant; anti-inflammatory; immunosuppressive; antiallergic;
KW antiasthmatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; pharmacogenomic.
XX
OS Homo sapiens.
XX
PN W0200268649-A2.
PD
XX
PF 06-SEP-2002.
XX
XX 31-JAN-2002; 2002WC-US002785.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278522P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288347P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.

30-MAY-2001; 2001US-0294473P.
08-JUN-2001; 2001US-0296964P.
18-JUN-2001; 2001US-0298959P.
19-JUN-2001; 2001US-0299324P.
13-AUG-2001; 2001US-0312020P.
16-AUG-2001; 2001US-0312889P.
16-AUG-2001; 2001US-0312908P.
21-AUG-2001; 2001US-0313930P.
28-AUG-2001; 2001US-0315470P.
31-AUG-2001; 2001US-0316447P.
07-SEP-2001; 2001US-0318115P.
07-SEP-2001; 2001US-0318118P.
12-SEP-2001; 2001US-0318740P.
19-SEP-2001; 2001US-0323379P.
18-OCT-2001; 2001US-0330245P.
18-OCT-2001; 2001US-0330308P.
14-NOV-2001; 2001US-0332701P.
(TCHE/) TCHERNEY V T.
(SPYT/) SPYTEK K A.
(ZERH/) ZERHUSEN B D.
(PATT/) PATTURAMAN M.
(SHIM/) SHIMKETS R A.
(LILL/) LILL L.
(GANG/) GANCOLLI E A.
(PADI/) PADIGARU M.
(ANDR/) ANDERSON D W.
(RAST/) RASTTELLI L.
(MILL/) MILLER C E.
(GERL/) GERLACH V.
(TAUP/) TAUPIER R J.
(GUSE/) GUSEV V Y.
(COLM/) COLMAN S D.
(WOLE/) WOLENC A R.
(PENA/) PENA C E A.
(FURT/) FURTVAK K.
(GROS/) GROSSE W M.
(ALSO/) ALSBROOK J P.
(LEPL/) LEPLY D M.
(RIEG/) RIEGER D K.
(BURG/) BURGESS C E.
Tchernev VT, Spytek KA, Zernusen BD, Patturajan M, Shimkets RA,
Li L, Gangoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE,
Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE,
Furtak K, Grosse WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
WPI: 2004-190039/17.
N-PSDB; ADN42419.
Isolated NOVX polypeptides and polynucleotides, useful for preventing
diagnosing and/or treating cancer, diabetes, cardiomyopathy and
atherosclerosis.
Claim 1; SEQ ID NO 302; 1309pp; English.

detecting the presence of NOVX in samples (e.g. by enzyme linked
immunosorbent assay (ELISA). The agents and methods may be used in this
way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
and/or atherosclerosis. The present sequence represents a NOVX protein.

Sequence 426 AA;

Query Match 91.1%; Score 2142; DB 8; Length 426;
Best Local Similarity 99.1%; Pred. No. 3,3e-186;
Matches 420; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARRTEPPDGGMGRVVLAFPOSALVGVRSFGVFVEFAAFEEQARAVSWIASIGI 60
DB 1 MARRTEPPDGGMGRVVLAFPOSALVGVRSFGVFVEFAAFEEQARAVSWIASIGI 60
QY 61 AVQFGSPVGSALSTKFGPRPVMTGTILALGMLLASFATSLTHLYISIGLLSGGMA 120
DB 61 AVQFGSPVGSALSTKFGPRPVMTGTILALGMLLASFATSLTHLYISIGLLSGGMA 120
QY 121 TPAFTLACISCYFSRRRLATGLATGVLSSTFTAPFPOMLSTHYARGSLIYSAISL 180
DB 121 TPAFTLACISCYFSRRRLATGLATGVLSSTFTAPFPOMLSTHYARGSLIYSAISL 180
QY 181 HLVACGALLRPPSLAEDPAVGGRPAQLTSLHHGPFRLRYTVALTLINTGYFIPIYLVAH 240
DB 181 HLVACGALLRPPSLAEDPAVGGRPAQLTSLHHGPFRLRYTVALTLINTGYFIPIYLVAH 240
QY 241 LODLDMDPLPAAFLLSVVAISDLVGRVYSGWIGDAVPGVTRLLMLWTTLTGVSIALP 300
DB 241 LODLDMDPLPAAFLLSVVAISDLVGRVYSGWIGDAVPGVTRLLMLWTTLTGVSIALP 300
QY 301 AQAPTALVALAVAGFTSGALAPLAFSVLPDLIGRRYICGILQWESIGLLGPPLS 360
DB 301 AQAPTALVALAVAGFTSGALAPLAFSVLPDLIGRRYICGILQWESIGLLGPPLS 360
QY 361 GYLIDVSGMYTASFVAGAFLLSGGILLTLPHFCFSSTTSGPODLVEALDTKVP 420
DB 361 GYLIDVSGMYTASFVAGAFLLSGGILLTLPHFCFSSTTSGPODLVEALDTKVP 420
QY 421 EGLE 424
DB 421 EGLE 424

RESULT 15
ADN42422
ID ADN42422 standard; protein; 426 AA.
AC ADN42422;
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XX
XX 17-JUN-2004 (first entry)
DT XX
XX Human novel protein NOV 96b.
DE XX
XX Human; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis.
XX
XX Homo sapiens.
OS
XX
XX US2004033493-A1.
PN
XX
XX 19-FEB-2004.
PD
XX
XX 31-JAN-2002; 2002US-00072012.
PF
XX
XX 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.

PR	09-FEB-2001	2001US-0267833P.
PR	15-FEB-2001	2001US-0268974P.
PR	26-FEB-2001	2001US-0271664P.
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PR	27-FEB-2001	2001US-0271855P.
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PR	02-MAR-2001	2001US-0273046P.
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PR	11-APR-2001	2001US-0282952P.
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PR	30-MAY-2001	2001US-0294473P.
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PR	18-JUN-2001	2001US-0296959P.
PR	19-JUN-2001	2001US-0296959P.
PR	13-AUG-2001	2001US-0299324P.
PR	16-AUG-2001	2001US-0312020P.
PR	16-AUG-2001	2001US-0312889P.
PR	21-AUG-2001	2001US-0312908P.
PR	28-AUG-2001	2001US-0313930P.
PR	31-AUG-2001	2001US-0315470P.
PR	07-SEP-2001	2001US-0316447P.
PR	07-SEP-2001	2001US-0318115P.
PR	12-SEP-2001	2001US-0318740P.
PR	19-SEP-2001	2001US-0323379P.
PR	18-OCT-2001	2001US-0330245P.
PR	18-OCT-2001	2001US-0330308P.
PR	14-NOV-2001	2001US-0332701P.
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Thu Sep 7 14:12:15 2006

us-10-654-428-2.rag

Page 16

job time : 199 secs

Thu Sep . 7 14:12:15 2006

us-10-654-428-2.ra1

Page 4

[illegible]

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US-09-949-016-6538
; Sequence 6538, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6538
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6538

Query Match      21.0%; Score 490; DB 2; Length 505;
Best Local Similarity 29.0%; Pred. No. 7.3e-39;
Matches 134; Conservative 75; Mismatches 213; Indels 40; Gaps 6;

Oy      1  MARRTEPPDGGGRVVVLSAFQSLVFGVLRSFCVFPFVVAPEQAAVSWIASIGI 60
Db      1  MPQALERADGSAWAVLLATMTVTOGITLGFPTTCIGITFELQWEPASNSFTSWPSIIIT 60

Oy      61  AVQFGSPVGSALSTRKFGPRPVVMNGILAAAGMLASFPATSTIHLIYLSIGLSGSGMAL 120
Db      61  AVLHAGAGLGLTLVERPCGRVTVVMJGVVLASLGMVASSFSHNLSQLYPTFAGFITGLGWCF 120

Oy      121  TFAPTLACLSYCFSSRRSLATGLALTGVLSSFTFAPEFQWLLSHYAMFGSLLSALSL 180
Db      121  TFAPTLACLSYCFSSRRSLATGLALTGVLSSFTFAPEFQWLLSHYAMFGSLLSALSL 180

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Db	121	SFOSSITVLCGFYVRRRVLANALAMSMVSGITITMPLSLRLENLGMRGFIIVGCGIFL	180
QY	181	HLVACGALLR-----PSTLAEEDPAVGGPPAQLTSLHHGPF--LRITYALT	225
Db	181	HCCICGAILRPVATSVAPETKECPPEPPETPPALGCLAAAGCTTIORHAFDILRH-----	234
QY	226	INTGYFA-----PYLHAIAHLQDDMDPPLPAFLSLVSAIIDLVGRRVSGW	271
Db	235	-NNGCYCYLLGVMMSVGLFPFLPQVFLVPIVRYAMMHSVDEQQALILSTIGFSNIFLRPLAGL	293
QY	272	LG--DAVPGCVTLIMLMTTLTGVSLAFVQAQPTLVALLAVAYGFTSGALAPLAEVL	329
Db	294	MACRPFAASHRKYLEFSLALILNGTITNIVCAASGDFWLVGVCILVSYMSMGIGALLFQVL	353
QY	330	PELIGTRRIICGLTLOMIESIGGLGLDLPRLSGYLDVSGNYTASFPVAGAFLLSGSGILL	389
Db	354	MDIVPMQGFPRALGFLFVLIDGLAFILISPLPAGLLDITNNFSYVFYMSFPLISPA--LF	411
QY	390	TLPHFECFSPTTSGPDVLVEALDTPKPLPKEGLEGGLNSTE	431
Db	412	MGGSFYALQCKEKGQKQAVADALDERDLFLAKQSPGKQSRSE	453

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RESULT 8
US-09-949-016-8809
/ Sequence 8809, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTNER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C0001307
/ CURRENT APPLICATION NUMBER: US/09/949, 016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ. ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8809
/ LENGTH: 521
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-8809

Query Match      21.0%; Score 490; DB 2; Length 521;
Best Local Similarity 29.0%; Pred. No. 7.6e-39;
Matches 134; Conservative 75; Mismatches 213; Indels 40; Gaps 6;

QY      1  MARTPEPDGNGRVVLSAFQSAIVFGVLRSGVFVEFVAAFEEOAAVSMIASIGI 60
      17  MPQALERADSGMVAWVLLATMTVGTLTGTGPTTCIGIFFTTELQWFOAKNSSETSWPSILT 76
DY
QY      61  AVQQFGSPVSSALSTKRGPPVYMTGGTILAAIGLLASFAISLTHYISIGILLSSGMAL 120
DY      77  AVAHMACPLTSLIVGRGCRVTWLGGVLLSGVASSFSHNLSQLFTTAGFTIGLGNCF 136
DY      121  TPAPTLACSCYFSRRRSRLATGALTIVGLSSFFFAEFQWLLSHYVWRGSLLVASLSL 180
DY      137  SFQSSIVLVGFYFRRRVLLANALASMGVSLGITLMPILSRLLBNLGNRGFFLVGGIFL 196
QY      181  HLYACGALLR-----PPSLAEDPAVGGPAAQLTSLLNHGF--LRYVALTL 225
DY      197  HCCICGAIIRPVATSVAPETKECPPEPPETPALGCLAACGRTIORHAFDILRH----- 250
QY      226  INTGYFI-----PYLHVAAHODDLMDPLPAFLLISVVAISDLVGRVSGM 271
DY      251  -NNGCYCYIILGKMSVIGFPLPQVFELVPYAMMHMSVDDQAAALLISIIIGFSNIPLRPLAGL 309
QY      272  LG--DAVPGVTRLLMLMTTLTGVSIALFPVAQAFTALVALAVAYGFTSGALAPLAFSVL 329

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Db 310 MAGPRAASHRRKYPFSLALLNGLTJNVCAASGDFWLVGICLAYSVMSGICALIQLVYL 369
QY 330 PELIGTRRIYCGILLOMIESIGILGPPLSGYLRDVSGNVTASFVVAAGFLLSGSILL 369
Db 370 MDIVPMQOPRAGLFTVLDGLAFILSPPLAGLLDITNNFSYVFYMSFPLISAA--LF 427
QY 390 TLHFFCFSTTSGPQDLVTEALDTKVPLEKXEGLEGJNSTE 431
Db 428 MGGSFYALOKKEQKQAVAADALERDLFLKADGPGKQSPRE 469

RESULT 9

US-10-074-547-5
Sequence 5, Application US/10074547
Patent No. 6989441
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A.J.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: 25466, A Human Transporter and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: MP12001-019PIRCPI(M)
CURRENT APPLICATION NUMBER: US/10/074,547
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/269072
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 487
TYPE: PRF
ORGANISM: homo sapiens
US-10-074-547-5

Query Match 20.3%; Score 473.5; DB 2; Length 487;
Best Local Similarity 26.6%; Pred. No. 2.8e-37;
Matches 122; Conservative 78; Mismatches 178; Indels 81; Gaps 5;

QY 5 TERPPGCGRNVVLSAFQOSALVFGVLSFGVFPEFVAPEEQARVSWIASIGIAVOQ 64
Db 12 TKLTDGGGMMIVIHFLVNVFVMGWTKTFPIFVFOEEFEGTSEQIGMISINSURF 71
QY 65 FGSFVGSALSTKFGPRPVMTGGILAAQMLASATSLTHLYSIGLSSGMAITRAP 124
Db 72 CAGPLVAILICILGKKTTSILGAFVVTGGYLISSWATSIPLCYTMGLLPGLGSAFLYOV 131
QY 125 TLACLSCFSSRRSLATGLTGVLSFTFAPFOWMLSHYAWGSLLVASLSHLVA 184
Db 132 AAVVTTKFKKRLALSTAIRSGMGL-TFLIAPFTKFLIDYDWTGAILFLGAILNLVP 190
QY 185 CGALLRPSLAEDPAVG-----GPRAOULTS----- 210
Db 191 GSMULRPIHKSENSNGIKKKGSSLSAAGPEAHATETHCHETESTIKDSTTOXAGLPSK 250
QY 211 -----LHNGP-----FLRYTVALTL 225
Db 251 NLTVSONOSEEFYQPNRNLILKSDSESDKVISWCKQLFDISLPNPFYIFTWSFLL 310
QY 226 INTGYFPIYHLVAHLODLDMDPLPAFLISVAISDLVGRVVGWLGDAVPGPVRLLM 285
Db 311 SOLAYFIPTFHLVARAKTLGIDIMDASYLVASVAGILETVSQIISGWADQNMIKKYHYHK 370
QY 286 LMTTLTGVSIALPVPVQAFTALVALAAVAGTSGALAPLAFSVLPPLIGTRRIYCGIGLL 345
Db 371 SYILGCTINLAPLATTFPLMTTYTICFAIFAGGYLALLPLVLDLCKNSTVNRFLGLA 430
QY 346 QMIESIGLGPPLSGYLRDVSGNVTASFVAG-AFLIS 383
Db 431 SFPAGMAVLSGPPIAGMLVDYTOTYNGSFYFSGICVILS 469

RESULT 10
US-09-949-016-10677

Sequence 10677, Application US/09949016
Patent No. 6812338
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10677
LENGTH: 492
TYPE: PRF
ORGANISM: Human
US-09-949-016-10677

Query Match 20.3%; Score 473.5; DB 2; Length 492;
Best Local Similarity 26.6%; Pred. No. 2.8e-37;
Matches 122; Conservative 78; Mismatches 178; Indels 81; Gaps 5;

QY 5 TERPPGCGRNVVLSAFQOSALVFGVLSFGVFPEFVAPEEQARVSWIASIGIAVOQ 64
Db 17 TKLTDGGGMMIVIHFLVNVFVMGWTKTFPIFVFOEEFEGTSEQIGMISINSURF 76
QY 65 FGSFVGSALSTKFGPRPVMTGGILAAQMLASATSLTHLYSIGLSSGMAITRAP 124
Db 77 CAGPLVAILICILGKKTTSILGAFVVTGGYLISSWATSIPLCYTMGLLPGLGSAFLYOV 136
QY 125 TLACLSCFSSRRSLATGLTGVLSFTFAPFOWMLSHYAWGSLLVASLSHLVA 184
Db 137 AAVVTTKFKKRLALSTAIRSGMGL-TFLIAPFTKFLIDYDWTGAILFLGAILNLVP 195
QY 185 CGALLRPSLAEDPAVG-----GPRAOULTS----- 210
Db 196 GSMULRPIHKSENSNGIKKKGSSLSAAGPEAHATETHCHETESTIKDSTTOXAGLPSK 255
QY 211 -----LHNGP-----FLRYTVALTL 225
Db 256 NLTVSONOSEEFYQPNRNLILKSDSESDKVISWCKQLFDISLPNPFYIFTWSFLL 315
QY 226 INTGYFPIYHLVAHLODLDMDPLPAFLISVAISDLVGRVVGWLGDAVPGPVRLLM 285
Db 316 SOLAYFIPTFHLVARAKTLGIDIMDASYLVASVAGILETVSQIISGWADQNMIKKYHYHK 375
QY 286 LMTTLTGVSIALPVPVQAFTALVALAAVAGTSGALAPLAFSVLPPLIGTRRIYCGIGLL 345
Db 376 SYILGCTINLAPLATTFPLMTTYTICFAIFAGGYLALLPLVLDLCKNSTVNRFLGLA 435
QY 346 QMIESIGLGPPLSGYLRDVSGNVTASFVAG-AFLIS 383
Db 436 SFPAGMAVLSGPPIAGMLVDYTOTYNGSFYFSGICVILS 474

RESULT 11
US-10-074-547-2
Sequence 2, Application US/10074547
Patent No. 6989441
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A.J.
APPLICANT: Millennium Pharmaceuticals Inc.
TITLE OF INVENTION: 25466, A Human Transporter and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: MP12001-019PIRCPI(M)
CURRENT APPLICATION NUMBER: US/10/074,547
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/269072

```

; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows
; SEQ ID NO 2
; LENGTH: 510
; TYPE: prt
; ORGANISM: homo sapiens
US-10-074-547-2

```

Query Match	20.1%;	Score 468;	DB 2;	Length 510;
Best Local Similarity	25.2%;	Pred. No. 1e-36;		
Matches 119;	Conservative 90;	Mismatches 166;	Indels 98;	Gaps 107;

[illegible]

RESULT 12
US-09-949-016-7542

Query Match	17.9%	Score 417.5;	DB 2;	Length 634
Best Local Similarity	27.5%;	Pred. No. 1.1e-31;		

Matches 114; Conservative 90; Mismatches 182; Indels 29; Gaps 91

```

QY      2  NARTPEPDGGMGRVVLVSAPFQSLVYGVGLARSGVFVEFVAAFEEQOARV-----SMIAS 57
Db      184  AAGFQPEPGGGGVVVVPAATCMGNSITFGHNSVGLYSLMILEEKERKROVERQOAMVGA 243
QY      58  IGIAVQOEGSPGVALSTFKFGRPPRVNWTGGILALGMLLASFATSLTHLYLSIGLSSG 117
Db      244  LAMGMIFPCSPVSLFTFDRLGCRITATAGAANAFIGLHTSSFTSSLSLRFTYGLIFGCG 303
QY      118  WALTEAPTLACLSCYFSFRRSLATGALTEVGSSFTFAFPFQWLLSHYAMRSSLVLVA 177
Db      304  CSFAFQPSLVIIGHFYORLTLANGVVASAGSIFSMSPFLIMLDDKIKLAQTFQVLST 363
QY      178  LSLHLVACCALLR--PSLAEDPAVGGPR-----AQLTSLDHGGPFIRYT-----VAL 223
Db      364  FMEVLMLSLTYRPLPFPSSQDTPESKRGVRTLHOFLAQLKRYNNMRVFORRTIRIAFGL 423
QY      224  TLINTEGYFPIYLVAHLAQDLMDPRLPAAPLLSV-VAISDLVGRVVSGMLGDAVPG- PVT 281
Db      424  AAAALGYFPFYVHLMKYVE--EFSBIKRYTWLVLCIGATGSLGSLVSGHISDSIPGLKRI 482
QY      282  RLIMLMTTLITGVSLALFVQAQAPRALVALVALAVGFTSG---ALAPLAFSVLDELIGTR 337
Db      483  YLVQVSLFLLIGLMSNMWIPLCRDFGLLIYVCLFELCDGFPTTIAAPLAF---ELVGPWO 538
QY      338  IYCGAGLLQMIESIGLGLGPPASGLVLRDSNGYVASFVVAAGAFLLSSGSLITLP 392
Db      539  ASQATIGLLGMALPMIAGPPLAGLLRNCPCDDHVAAYFAGVPPRIICAVILFVP 593

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RESULT 13
US-10-074-547-4
; Sequence 44, Application US/10074547
; Patent No. 6988441
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: 25466, A Human Transporter and Uses
; TITLE OF INVENTION: Therefore
; FILE REFERENCE: MP12001-019PRCP1(M)
; CURRENT APPLICATION NUMBER: US/10/074,547
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/269072
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 611
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus
US-10-074-547-4

```

Query Match	17.1%;	Score 398.5;	DB 2;	Length 611;
Best Local Similarity	21.7%;	Pred. No. 7.5e-30;		
Matches 133;	Conservative 81;	Mismatches 141;	Indels 259;	Gaps 14

```

QY      20 AFQGSALVEGILRSNG-VFVEFVFAAFEOAARVSM--IASIGIVAOQFSGVSGSLSTRK 76
Db      1 SFLNGFIDGPPKSTGGLIFREELQEEPAASNETSMDSISLLAVLVEAGCLASLTVNR 60

QY      77 FGPRPVVVTGGIILAALMLLASFATSLTHLYLSIGLSSGGMALTFAPTLACLSCYFSRR 136
Db      61 FGRRLVITAGGLIASSGCMWLASFANISELYLTFVIGLGAFTYLPALVITTSYFEKK 120

QY      137 RSLATGALTVGGLSFTFAPF--FQWLISHYA--WRQSLILIVS-----ALSLH 181
Db      121 RSLATGIVAGSGVGTFFVLIAPNPQFILIENYNGSKRRALLFFGGMGYVIAIMSVAVIYN 180

QY      182 LVAGCALLRP-----PGL 194

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Db      181 CCIAGALFRPLPSEKVKOTKLAKAEPEKALKSKENASESIDSIRSAKAIVSPETPAL 240
QY      195 AEPBAGGPPRAOTSLHHG-----PFLRY--TVALTINTGYFI 232
Db      241 SLSPELTPKKQOQLKLTSTRSSNNAKLIDFVLKDARGFLLYASGSLASIGTQFL 300
QY      233 P-----YLAHVAA 240
Db      301 PGSLFVNFPAKSLGSELSVSKKEAFLSLIGDSDKEFGGIFARPATLLSLPGVAN 360
QY      241 LQD-----LMDPLPAAF-- 253
Db      361 LKETSRRPULIYLLSLCSIVAVVINGILSLASALAGSRKREKKISMIDKIELKSTFWG 420
QY      254 -----LLSVY 258
Db      421 LPLFSLFFGVGFGSKKAVVILALGFLFLFSLIYALPVVGLQKYSALGLTETDASTLIEAI 480
QY      259 AISDIVGRVVSQWLGDAVPGPVTRLLMLMTTTCVSLALPPVAQAPPAVALA----- 311
Db      481 AVLNTIGRPLAGLADTKRKLAIYVLSLGLFVAFAPLA--TIFGLAFYCVLFG 537
QY      312 ----VAY--GFTSGALAPLAFSVLPBELIGTRRIYIGLGLQMIIESIGLLAPPLSGYL 363
Db      538 SIVFLAYAFKFGCKGKSYIALTSVIAVDLTGLDKLSNAFGLLLFQGVATLVGPPIAGLL 597
QY      364 RDVSGNYTASFVVA 377
Db      598 KDLTGSGVKSFYFA 611

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RESULT 14
US-09-270-767-44472
; Sequence 44472, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 1999-03-17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 44472
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44472

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Query Match      16.1%; Score 376; DB 2; Length 480;
Best Local Similarity 37.3%; Pred. No. 8.1e-28;
Matches 69; Conservative 44; Mismatches 72; Indels 0; Gaps 0;

QY      7 PPDCGWRVVVLSAFQOSALVFGVLRSPGFVFEEVFAFEQARVSIASIGIAVQFG 66
Db      93 PPDCGYGVVLCFASFCMCMIVDGIATYTGITLLEEFVAFHEGKGTVAWVGSLGAVYISA 152
QY      67 SPVGSALSTRKGPVPVMTGILALGMLLASFATSLTHLYLSIGLLSGSGMALTFAPTL 126
Db      153 GPVLSALANKYGCRAVCIAGSIICIAFVLTSTFNVMMLATYGFPGGFGFGIMYIPAV 212
QY      127 ACLSCYFSRRSLATGALTGVLGSLTFPAPFQWMLSHYAMRGSLLVLSLHLVACG 186
Db      213 VAVGYVETKRSATGIAVCGSGGTFAFAPLATLYLLEEGMKVALLIFAGLILNCAIFG 272
QY      187 ALLRP 191
Db      273 AMMRP 277

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RESULT 15
US-09-328-352-4392
; Sequence 4392, Application US/09328352

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```

; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER.
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4392
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4392

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```

Query Match      15.0%; Score 350; DB 2; Length 429;
Best Local Similarity 29.0%; Pred. No. 2.3e-25;
Matches 117; Conservative 69; Mismatches 171; Indels 46; Gaps 16;

QY      13 GRVVVLSAFQOSALVFGVLRSPGFVFEEVFAFEQARVSV--IASIGIAVQ--FGS 67
Db      43 GSAILP-----ALSIGVRHGFGLVLPMSHF-----GCGHVFSIALAMONLIWGA 89
QY      68 --PVGSALSTRKGPVPVMTGILALGMLLASFATSLTHLYLSIGLLSGSGMALTFAP 124
Db      90 IOPFTGAIADKYGSKVVTGGLTYTLGLLMAFSSVLIINLSGLIIGLALSAITSFTV 149
QY      125 TLACLS-CYFSRRSLATGALTLTGVLGSSFTFAPFQWMLSHYAMRGSLLVLSLHLV 183
Db      150 LLSAVGRAPPEKRSMAANGISASAGSFGCFIMLPSTLLTLTKVG--SSALMWSALLIALI 208
QY      184 ACGA-LRPPSLAEDPAVGPPRAOTSLDH---HGPFARYVALTLINTGYFIYL--H 236
Db      209 IPLAMMLGPNQPPKAIAPQLTFKQVLHARKHKE--WMLAGFLVCGFQVFLGVH 266
QY      237 LVANLQDDMPRLPRAFLSVVAISDLVGRVVSQWLGDAVPGPVTRLLMLMTTTLGVSIA 296
Db      267 LPGYLDHGFATYTGVLALVGLFNITVGTGAGMLGDRFSKP--KLMLYSGSGIAI 324
QY      297 LPVVAQAPTAVALAVAVGFTSGAL---APLAFSVLPBELIGTRRIYIGLGLQMIIESIG 352
Db      325 AFLPLPSTYTV--YAFGIIMGLMLSTVPLTINGIVANMGVXYLSMLSGIVFTHQVG 381
QY      353 GLCPPLSGYLRDVSQNYTASFVVAQAFLLSGSGLILTLPHFF 395
Db      382 SFFGWLGGVNHDLTGNYNAIWLCSIAL-----SILGVYHFF 419

```

Search completed: September 7, 2006, 13:08:58
Job time : 52 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2006, 13:02:26 ; Search time 41 Seconds

(without alignments)
1072.465 Million cell updates/sec

Title: US-10-654-428-2

Sequence: 1 MARRTEPPDGGMGWVVA.....SLTAPGLLPRLGHRTPV 457

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591	25.4	484	2	A55626 monooxycarbonate tr
2	564	24.2	542	2	JCS507 monooxycarbonate tr
3	555.5	23.8	494	2	A44458 probable transp
4	546	23.4	494	2	JC4399 monooxycarbonate tr
5	540	23.2	500	2	A55568 monooxycarbonate tr
6	482.5	20.7	598	2	T32430 monooxycarbonate tr
7	463.5	19.9	556	2	T16790 monooxycarbonate tr
8	417.5	17.9	613	2	I39295 monooxycarbonate tr
9	370.5	15.9	397	2	G69295 oxalate/formate an
10	368.5	15.8	402	2	F95874 probable transp
11	368.5	15.8	596	2	T23985 hypothetical prote
12	342	14.7	571	2	T33941 hypothetical prote
13	314.5	13.5	800	2	T16564 hypothetical prote
14	290.5	12.5	399	2	F83484 hypothetical prote
15	288	12.4	410	2	G82445 probable MFS trans
16	280	12.0	406	2	AG2704 MFS permease (limp
17	250.5	10.7	407	2	G97486 probable MFS trans
18	250.5	10.7	407	2	AC1346 antiporter protein
19	249.5	10.7	416	2	G69748 conserved transmem
20	249.5	10.7	405	2	H81995 probable transmem
21	245.5	10.5	407	2	AR1716 antiporter protein
22	245	10.5	418	2	F83986 transp
23	241	10.3	426	2	T50944 transporter BH2694
24	238.5	10.2	402	2	S47768 hypothetical prote
25	236	10.1	673	2	S59263 hypothetical 43K p
26	231	10.0	400	2	H91182 probable resistanc
27	231	10.0	400	2	D66029 probable resistanc
28	230.5	10.0	405	2	T44249 transport protein
29	210.5	9.8	431	2	AB2949 MFS permease (mono

30	229.5	9.8	433	2	H98333 hypothetical prote
31	228.5	9.8	398	2	AD0828 probable transmem
32	226.5	9.7	430	2	S74039 hypothetical prote
33	226	9.7	473	2	S38065 hypothetical prote
34	225	9.7	444	2	E83033 probable MFS trans
35	222	9.5	419	2	H83965 hypothetical prote
36	220	9.4	420	2	H69250 oxalate/formate an
37	218	9.4	388	2	AG3307 oxalate/formate an
38	208	8.9	373	2	S00656 hypothetical prote
39	206	8.8	408	2	H95184 oxalate/formate an
40	206	8.8	408	2	H98051 major facilitator,
41	205	8.8	412	2	T37042 probable nitrate/n
42	201	8.6	501	2	S66816 probable membrane
43	199.5	8.6	371	2	B90267 transport protein,
44	199.5	8.6	807	2	T20080 hypothetical prote
45	196.5	8.4	428	2	A75423 multidrug resistanc

ALIGNMENTS

RESULT 1

A55626

monooxycarbonate transporter MCT2 - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C>Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 18-Sep-1998

C:Accession: A55626

J. Garcia, C.K.; Brown, M.S.; Pathak, R.K.; Goldstein, J.L.

J. Biol. Chem. 270, 1843-1849, 1995

A:Title: CDNA cloning of MCT2, a second monooxycarbonate transporter expressed in differ

A:Reference number: A55626; MID:95130566; PMID:7829520

A:Accession: A55626

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-484 <GAR>

A:Cross-references: UNIPARC:UPI0000178664; GB:L31957

A:Superfamily: monooxycarbonate transporter MCT2

C:Keywords: transmembrane protein

Query Match 25.4%; Score 591; DB 2; Length 484;

Best Local Similarity 33.1%; Pred. No. 9.7e-33;

Matches 135; Conservative 72; Mismatches 175; Indels 26; Gaps 4;

QY	7	PPDGGMGWVVA	LSAF	FFQSLAV	GVLR	SGVF	FEVFA	FEQAAR	VSMTAS	IGIVQ	66
DB	14	PPDGGMGWVVA	GA	AFIS	IGFSY	APKAV	TVF	FKIQI	FOAS	YSIA	WISSIM
QY	67	SPVGSAL	STK	GGPRPV	VTG	IGIL	AL	GM	LAS	PAT	SLTH
DB	74	GPISSV	VNN	NGSP	RVV	IIG	LCT	GM	ILAS	FNS	VLE
QY	127	ACLS	CF	RR	SL	AT	GL	AT	GV	LS	ST
DB	134	TIIG	KY	RR	RR	PM	ANG	AM	GS	VF	LS
QY	187	ALL	RP	---	PS	LA	ED	PA	VG	PP	RA
DB	194	CLMR	PV	OT	SP	RR	SK	SK	SV	SS	QD
QY	224	TL	INT	GF	PI	YL	LV	AL	QD	LD	WD
DB	254	VIM	FG	FA	IT	IL	AV	AD	KV	DE	YNA
QY	282	RL	ML	MT	TL	TV	GS	LA	FP	VA	QA
DB	314	YF	SP	FA	IV	GT	GI	CH	IL	CP	LD
QY	342	IG	LO	WIE	S	IG	IG	LP	SG	YL	PD
DB	374	VG	LA	IV	EC	CP	VL	GP	PL	AG	KV

UC5507
monocarboxylate transporter 3 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C:Accession: UC5507
R:Yoon, H.; Fanelli, A.; Grollman, E.F.; Philp, N.J.
Biochem. Biophys. Res. Commun. 234, 90-94, 1997
A>Title: Identification of a unique monocarboxylate transporter (MCT3) in retinal pigment epithelial cells
A:Reference number: UC5507; MUID:97312526; PMID:9168967
A:Accession: UC5507
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1..542 <YOO>
A:Cross-references: UNIPROT:O90632; UNIPARC:UP00000171286; GB:U15685
A:Experimental source: retinal pigment epithelial cell
C:Comment: This protein regulates lactate levels in the interphotoreceptor space.
C:Superfamily: monocarboxylate transporter MCT2
C:Keywords: phosphoprotein
F:1/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F:21/Binding site: phosphate (Thr) (covalent) (by cAMP- and cGMP-dependent kinases) #status predicted
F:234,467/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:262,526/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 24.2%; Score 564; DB 2; Length 542;
Best local similarity 30.5%; Pred. No. 7,3e-31;
Matches 146; Conservative 82; Mismatches 185; Indels 66; Gaps 9;

Oy C EPPPCGWGRVVVLSAFQSSALVFGVLRSNGVFVEFVAAPFEQARVSIMASIGIAVOGF 65
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db KPPDGGMGWIVLPGCFVTITGSIAEPKAVSYFKELMDPHVGSIDTAMISSIMLAMLYG 75
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy GSPPVASASTKCPRPVVMVTGILAAQLMLASFATSLTHLYLSIGLLSGSWALTFAPT 125
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db TGTTCSIMWNOFCGRPVMLIGGLASSGMILLASFTTNIIIEIYLTAGVLTGAGMALNFPS 135
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy LACISICYSRRSRSLATGLALTGVGLSFTFAFPOMLLSHVAKRSSLVLSAHLVAC 185
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db LIMIGTYDKRRPLNGLAAMGPSVFLSSLPLGCVLLEKPKMGRLIMGILLNCCTC 195
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy LAGELRP-----PSLAED-----PAV-----GPRA 205
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db CAVERPDLDAQMRKEKADKYEAKEMPMGSKSEGISTDGTCKTKAKKKPKKGKL 255
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy QLTSLHMHGPRPYVALTLINTGYFIPLYHLVAHLQDLLDMDPLPAELLSSVAISDLVG 265
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db LDPSIFSRGFIITYISKFILVLGLFVPILLVNAYAKDTGVDDTAELLSTIGPIDIFA 315
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy RVAGS-----WLGAAGVGPVTRLLMTTLTGVSALFPAVAQAATALVALAVAAGTFIS 319
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db RPACGMVAAGLKVRPHV--AYLFSPALRFNGLLDISAR--ASNTGTVIFCVDFGISYG 371
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy ALAPAFAFVLPDLICTRIYCGLLGLOMTESIGLLGPLSGCYLRDVSGNYTASFVAGA 379
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db MWGALOFEVLAIVOSQKPSSAIGLVLLIEARVAVLIGPSSAGRVDALKNEVEPIYLAGS 431
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy FLSSSGGLTLTPHFQCFSTTSGPDVTEALDTKVLPKRGEGLGNSTESGESQS 438
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db EVVL-SALFLMAVATYCCLNRGKTP-----PPEKNPASGAGSDTE---EAS 474
||| ||| ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 3
A44458
probable transporter Mev - Chinese hamster
N:Alternate names: mectl
C:Species: Citellus griseus (Chinese hamster)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A44458; I48115
R:Kim, C.M.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 267, 2313-2321, 1992
A>Title: cDNA cloning of MEV, a mutant protein that facilitates cellular uptake of mevalonate
A:Reference number: A44458; MUID:93054638; PMID:1429658
A:Accession: A44458
A>Status: preliminary; not confirmed with conceptual translation

A:Molecule type: nucleic acid
A:Residues: 1-494 <KIM>
A:Cross-references: UNIPARC:UPI000017072E; GB:M97382; NID:g191143; PIDN:AAB59630.1; PID:G
A:Experimental source: CHO clone met-18b-2
A>Note: Sequence extracted from NCBI backbone (NCBIF_118221)
R.Garcia, C.K.; Goldstein, J.L.; Pathak, R.K.; Anderson, R.G.W.; Brown, M.S.
Cell 76, 865-873, 1994
A>Title: Molecular characterization of a membrane transporter for lactate, pyruvate, and
A:Reference number: A49951; MUID:94170387; PMID:8124722
A:Accession: U48115
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-359, 'F', 361-494 <RES>
A:Cross-references: UNIPARC:PI000012F3BF; GB:I25842; NID:g472332; PIDN:AAB59731.1; PID:G
C:Superfamily: monocarboxylate transporter MCT2

Query Match 23.8%; Score 555.5; DB 2; Length 494;
Best Local Similarity 31.8%; Pred. No. 2,5e-30;
Matches 135; Conservative 64; Mismatches 182; Indels 43; Gaps 5;

OY PPDGMGVVVLAFPGQALVFGLRSFCGFVEFAFEEDQARYSWISIGIAVOFG 66
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB PPDDGMGAHVAVGATISGFSTAFPKSTIVFKETICINATTSEVSMIAVAYAG 72
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY SPVGSALSTKGPPRPVVMTGTILALGMLASFATSLTHLYLSIGLSSGWALTAPTL 126
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB GPISSVLVNKXGRSRPMIAGCGCLSGGGLIASPCNTVGELYLCIGVIGGLAFNLDPAL 132
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY ACLCSFYRRRLSANGLTGVGLSSFPAFPQQMLSHYAMGSGLLVVALSHLVACG 186
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB TWIGYFFPKKPLANGLAMAGSPVFLSTLPANQAEPFGIFMGWGSPFLIGLLNCCVAG 192
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY ALLRP-----PSLA-----DPAVGGPRAOTLSLH----- 212
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB SLMRIRGPCKTEKLKSKEIOEGAKSEANDMDMGSFKGEKRSVLQTINKFLDSLFA 252
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY HGPFLLRYTVAULTINTGYFIPLYHLVAHLQDLDMDELPAFLLSVAASIDLVRVSGWL 272
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB HRGFLLYLSGNVMFMFGFTPLVPLFSNYGSKQSYSEKSAFLSLIAFVDMAVRPMGLA 312
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY 273 GDA--VPQPVTRLMLMTTLTGVSALFPVQAQPTLVALLAAVAYGTFSGALAPLAFSVLR 330
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 313 ANTKWIRPRIQYFFAASVAVANVCHELLAPLSTSYIFCIIYAGVFGFACGMLSVELFTLM 372
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY 331 ELIGTRRIYCGGLQMIESIGLLGPPPLSGYLRDVSNYTA SF-----VVA GAFLLS 383
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 373 DLVGQRSSANGVLTIVDECPVLLGPRLLGLRNDFMYGDIXKYTMACGVLIILINGIYIFI 432
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY 384 GSGI 387
 ||||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 433 GMGI 436

RESULT 4
UC4399
monocarboxylate transporter - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: JC4399
RT:Kangana, H.; Tanai, I.; Inaba, S.; Sai, Y.; Higashida, H.; Yamamoto, H.; Tsuji, A.
Biochem. Biophys. Res. Commun. 217, 370-377, 1995
A>Title: cDNA cloning and functional characterization of rat intestinal monocarboxylate t
A:Reference number: UC4399; MUID:96095680; PMID:8526936
A:Accession: UC4399
A:Molecule type: mRNA
A:Residues: 1-494 <TA>
A:Cross-references: UNIPROT:P53987; UNIPARC:UPI000012F3C2; GB:D63834; NID:g1199781; PIDN
A:Experimental source: Small intestinal mucosal cells
C:Genetics:
A:Gene: mct1
C:Superfamily: monocarboxylate transporter MCT2
C:Keywords: intestine; transmembrane protein
F:16-36/Domain: transmembrane #status predicted <TM>

F:60-81/Domain: transmembrane #status predicted <TM2>
 F:87-105/Domain: transmembrane #status predicted <TM3>
 F:112-136/Domain: transmembrane #status predicted <TM4>
 F:145-172/Domain: transmembrane #status predicted <TM5>
 F:176-195/Domain: transmembrane #status predicted <TM6>
 F:196-225/Region: hydrophilic
 F:226-280/Domain: transmembrane #status predicted <TM7>
 F:292-314/Domain: transmembrane #status predicted <TM8>
 F:322-342/Domain: transmembrane #status predicted <TM9>
 F:346-368/Domain: transmembrane #status predicted <TM10>
 F:380-402/Domain: transmembrane #status predicted <TM11>
 F:416-439/Domain: transmembrane #status predicted <TM12>

Query Match 23.4%; Score 546; DB 2; Length 494;
 Best Local Similarity 30.2%; Pred. No. 1,1e-29;
 Matches 145; Conservative 66; Mismatches 215; Indels 54; Gaps 7;

```

QY 7 PPDGKGRVVVLSAFQSGALVFGVLSFGVFEFVAFAFEQARVSMIASIGIAVOQFG 66
D 13 PPDGGMWAVVGAFAISIGFSYAFPKSITVFFKEIGIFHATTSSEVSWISSIMLAVMYGG 72
QY 67 SPVGSALSTKFGPRPVMTGIIAALGMLASFSATSLTHLYSIGLSSGMAITFEAPTL 126
D 73 GPISILVKKYSGSRVMTAGGCLSGCGLIASFNCNTVOELVFCIGVIGIGLAFNINPAL 132
QY 127 ACTSCYFSRRSLATGALTGVLSFTFAPFPQWMLSHYARGSLIVSALSLLHVACG 186
D 133 TWIKYFYKRRPLANGLAMAGSPVFLCTIAPLNOQVFGIFGWRGSEFLILGILLNCVAG 192
QY 187 ALMRP-----PSIAE-----DPAVGGPRAQL-----TSLAH 212
D 193 SLMRPFGPOOGKVEKLSKESLQEAGKSDANTDLIGSGPKGELSTFQVYNNKFLDISLPT 252
QY 213 HGFPLRYVALTLINGYFIPRYLHVLAHODLDMDPLPAFLISVAISDLVGRVNSGM 272
D 253 HNGFLIYKGVNVVMEFGLTPTPLVFLSNYKSKIFSEKSAFLISILAFDVMARPSMGIA 312
QY 273 GGA--VPCGVTRLMLMTLTGVSALFPVAQAPTLVALVAVGTSGALPLAFSVIP 330
D 313 ANTRWTRPRVQYFPFASVAVANGCHLAPLSTTYVGCYAVGFGAFGMLSSVFEETLM 372
QY 311 ELIGRRRLYCGILQMLQIESIGLIGPPLSGYLDVSGNYTASF-----VWAGAPLIS 383
D 373 DLVGRFRRSSAVGLVTIVECCPVLLGPPLGLRLNDMYDKYTTACGVIILIAGLYIFI 432
QY 384 GSGI--LTLPHFPCFTTSGPOLVTEAD-----TKVPLPREGLEGGLNSTES 432
D 433 GMGINYLVAKEQAEKKRDKEDSTSDYDEKPKTKMETQSPAPLQNSGDPAREES 492

```

RESULT 5

A:55568

monocarboxylate transporter 1 - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: A55568; T47157

R/Garcia, C.K.; Li, X.; Luna, J.; Francke, U.

A>Title: cDNA cloning of the human monocarboxylate transporter 1 and chromosomal localiz

A/Reference number: A55568; MUID:95137602; PMID:7835905

A/Accession: A55568

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-500 <CAR>

A/Cross-references: UNIPROT:P53985; UNIPARC:UPI000016AD1B; GB:U31801; NID:9561721; PIDN:

A/Note: authors translated the codon GCA for residue 279 as Asp

R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Well, B.; Wiemann, S.

A/Reference number: Z24379

A/Accession: T47157

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-479; 'A', 481-500 <AAA>

A/Cross-references: UNIPARC:UPI000012F3C0; EMBL:AL162079
 A/Experimental source: adult melanoma (Wewo cell line); clone DKFZp762B2310
 C/Genetics:
 A/Gene: GDB:SLC16A1, MCT1
 A/Cross-references: GDB:373211, OMIM:600682
 A/Map position: 1p13.2-1p12
 A/Note: DKFZp762B2310.1
 C/superfamily: monocarboxylate transporter MCT2

Query Match 23.2%; Score 540; DB 2; Length 500;
 Best Local Similarity 30.6%; Pred. No. 2,8e-29;
 Matches 133; Conservative 64; Mismatches 181; Indels 56; Gaps 6;

```

QY 7 PPDGKGRVVVLSAFQSGALVFGVLSFGVFEFVAFAFEQARVSMIASIGIAVOQFG 66
D 13 PPDGGMWAVVGAFAISIGFSYAFPKSITVFFKEIGIFHATTSSEVSWISSIMLAVMYGG 72
QY 67 SPVGSALSTKFGPRPVMTGIIAALGMLASFSATSLTHLYSIGLSSGMAITFEAPTL 126
D 73 GPISILVKKYSGSRVMTAGGCLSGCGLIASFNCNTVOELVFCIGVIGIGLAFNINPAL 132
QY 127 ACTSCYFSRRSLATGALTGVLSFTFAPFPQWMLSHYARGSLIVSALSLLHVACG 186
D 133 TWIKYFYKRRPLANGLAMAGSPVFLCTIAPLNOQVFGIFGWRGSEFLILGILLNCVAG 192
QY 187 ALMRP-----PSIAE-----DPAVGGPRAQL-----TSLAH 212
D 193 SLMRPFGPOOGKVEKLSKESLQEAGKSDANTDLIGSGPKGELSTFQVYNNKFLDISLPT 252
QY 213 HGFPLRYVALTLINGYFIPRYLHVLAHODLDMDPLPAFLISVAISDLVGRVNSGM 272
D 253 HNGFLIYKGVNVVMEFGLTPTPLVFLSNYKSKIFSEKSAFLISILAFDVMARPSMGIA 312
QY 273 GGA--VPCGVTRLMLMTLTGVSALFPVAQAPTLVALVAVGTSGALPLAFSVIP 330
D 313 ANTRWTRPRVQYFPFASVAVANGCHLAPLSTTYVGCYAVGFGAFGMLSSVFEETLM 372
QY 311 ELIGRRRLYCGILQMLQIESIGLIGPPLSGYLDVSGNYTASF-----VWAGAPLIS 383
D 373 DLVGRFRRSSAVGLVTIVECCPVLLGPPLGLRLNDMYDKYTTACGVIILIAGLYIFI 432
QY 384 GSGI--LTLPHFPCFTTSGPOLVTEAD-----TKVPLPREGLEGGLNSTES 432
D 433 GMGINYLVAKEQAEKKRDKEDSTSDYDEKPKTKMETQSPAPLQNSGDPAREES 492

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RESULT 6

T32430

hypothetical protein C10E2.6 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T32430

R/Wohlmann, P.; Sansone, J.

A/Description: The sequence of C. elegans cosmid C10E2.

A/Reference number: Z21165

A/Accession: T32430

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-598 <MOH>

A/Cross-references: UNIPROT:O17328; UNIPARC:UPI000017B768; EMBL:AF026202; PIDN:AA871245.1

A/Experimental source: strain Bristol N2; clone C10E2

A/Genetics: CESP:C10E2.6

A/Map position: X

A/Intons: 53/3; 103/2; 145/2; 476/3; 569/3

Query Match 20.7%; Score 482.5; DB 2; Length 598;
 Best Local Similarity 23.4%; Pred. No. 2,6e-25;
 Matches 135; Conservative 75; Mismatches 181; Indels 185; Gaps 8;

```

QY 7 PPDGKGRVVVLSAFQSGALVFGVLSFGVFEFVAFAFEQARVSMIASIGIAVOQFG 66
D 13 PPDGGMWAVVGAFAISIGFSYAFPKSITVFFKEIGIFHATTSSEVSWISSIMLAVMYGG 72
QY 67 SPVGSALSTKFGPRPVMTGIIAALGMLASFSATSLTHLYSIGLSSGMAITFEAPTL 126
D 73 GPISILVKKYSGSRVMTAGGCLSGCGLIASFNCNTVOELVFCIGVIGIGLAFNINPAL 132
QY 127 ACTSCYFSRRSLATGALTGVLSFTFAPFPQWMLSHYARGSLIVSALSLLHVACG 186
D 133 TWIKYFYKRRPLANGLAMAGSPVFLCTIAPLNOQVFGIFGWRGSEFLILGILLNCVAG 192
QY 187 ALMRP-----PSIAE-----DPAVGGPRAQL-----TSLAH 212
D 193 SLMRPFGPOOGKVEKLSKESLQEAGKSDANTDLIGSGPKGELSTFQVYNNKFLDISLPT 252
QY 213 HGFPLRYVALTLINGYFIPRYLHVLAHODLDMDPLPAFLISVAISDLVGRVNSGM 272
D 253 HNGFLIYKGVNVVMEFGLTPTPLVFLSNYKSKIFSEKSAFLISILAFDVMARPSMGIA 312
QY 273 GGA--VPCGVTRLMLMTLTGVSALFPVAQAPTLVALVAVGTSGALPLAFSVIP 330
D 313 ANTRWTRPRVQYFPFASVAVANGCHLAPLSTTYVGCYAVGFGAFGMLSSVFEETLM 372
QY 311 ELIGRRRLYCGILQMLQIESIGLIGPPLSGYLDVSGNYTASF-----VWAGAPLIS 383
D 373 DLVGRFRRSSAVGLVTIVECCPVLLGPPLGLRLNDMYDKYTTACGVIILIAGLYIFI 432
QY 384 GSGI--LTLPHFPCFTTSGPOLVTEAD-----TKVPLPREGLEGGLNSTES 432
D 433 GMGINYLVAKEQAEKKRDKEDSTSDYDEKPKTKMETQSPAPLQNSGDPAREES 492

```

```
Dh 17 PRDGGKGVVVLGSFFVHVFADGFFVYSPGVLEVTELMEEFHASNTMAALLISLTGTLTGS 76
Qy 67 SSVVSTSLSTKFGPRPVVMTGGILALGMLLASFATSLTHLYLSIGLSSGGMALTFAPTL 126
Dh 77 GPLASAVCNKRYGCRITTTTGAGVAFVGCALSTFATMMHIVITVYIMGTGRLMCPAI 136
Qy 127 ACLSCYFSRRSLATGALTGVGLSFTFPAFFOMLSHYAMRGSLLLVSALSLHVACG 186
Dh 137 ::::THYFENKRSLATGIAVAGVGTVPFAPINAFPLNNYGMRSVFLEFLILCALCG 196
Qy 187 A-----LLRPSL----- 194
Dh 197 ATFAPLEFALVPDEEVEVDEVDVKKYTAANEHEGKATLLSPSLERSMSGSGVQ 256
Qy 195 -----AEDP----- 198
Dh 257 KAGEKIRPASSKCAVDVESQPRSRGTGGERDSGYLNKRVFTTGSISNVAEREDBDKX 316
Qy 199 -----AVGPPRAQLT----- 208
Dh 317 RSTGSLHGRHTTGSIPAHSTGRLDVREGSEEDSKAMDISKTNGTNDTNEGKMK 376
Qy 209 -----SLHHGPRLRYVALTLINTGYFIPYLIHVAHLODMDPLPAALFLSVAI 260
Dh 377 TISNKLSTLELLLEPTFLFALISNLTLSVGNSPLYPFLPHATKIGLEPIGSKVLSAFGV 436
Qy 261 SDLVGRVSGMLGP---AVPGPV---TRLMLW-----TLTGVSALFPFAQPTALVA 309
Dh 437 SNTVGRITFGVAVDHLKPLPEGINDTARKRLMYNLSLTICGLTYFCQFQNFPLAT 496
Qy 310 LAVAVGFTSCLALPAFVSVPPELIGTRRIYCGGLCOMISIGLCLPPLSGYIRDVSGN 369
Dh 497 YSALFCSIASIYICLTSLVILDLGLDKLTNAFGLLLMQGVGVFQPVSGYLADMTGN 556
Qy 370 YTAFTVAVGA-----FLSSGGLTLTPHFPCF 397
Dh 557 YTLSPVTCGVNLTLPLOFHLSSGFLVHFVHYLGF 592

RESULT 7
T16790
hypothetical protein T02G5.12 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence-revision 20-Sep-1999 #text-change 09-Jul-2004
C/Accession: T16790
R/Parley, A.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid T02G5.
A/Reference number: Z18577
A/Accession: T16790
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-556 <PAU>
A/Cross-references: UNIPROT:O22109; UNIPARC:UP1000007FBA4C; EMBL:U41105; NID:g1086772; P1
A/Gene: CESP:T02G5.12
A/Introns: 50/3; 100/2; 142/2; 184/3; 350/1; 435/3; 528/3

Query Match 19.9%; Score 463.5; DB 2; Length 556;
Best Local Similarity 25.4%; Pred. No. 4.7e-24;
Matches 134; Conservative 76; Mismatches 178; Indels 139; Gaps 9;
```

```
Qy 175 -----VSALSLHY-----ACGA- 187
Dh 194 DGEYNDVFEDEVKKIDYNKRFEKVSLSLPQVRSNSCCDIOKNQNHARPSSVAV 253
Qy 188 -----LLRP-----PSLAE--DP-----AVGPPRAQLTSLH 212
Dh 254 DLBPRLPRCGTIGERNSGYLNKRDVFTTGSISNVAERAPDKXRSGLHTALNHTH 313
Qy 213 H-----GPRLTVALTLINTGYFIPYLIHV 238
Dh 314 HGTGVDDRESGHCDDQSLDGMNEKETDFMDIDEGTLTFLAISNLTLSVGNSPLYPFL 373
Qy 229 AHLQDMDPLPAALFSLVVAISDLVGRVSGMLCD-----AVGPPTRLMLW----- 287
Dh 374 LAVTNILDNNVSGNLTISVGTANTGRLIFGVVADQKLPAPAGLDDTARRRLMYNIS 433
Qy 288 TLLTGVSALFPFAQPTALVALAVAGFTSGALPAFVSVPPELIGTRRIYCGGLIOM 347
Dh 434 LTTCGIVTAPCYKFDGYTLIDLIYAVLPFTTASIVCLSVILVDLGLDKLTNAFGLLL 493
Qy 348 IESIGLGPPLSGYLRDVSGNYTASFYVAGAFLLSGGILTLPHF 394
Dh 494 WQGVGTIVGLVSGYLADLTGNVYTLSPFCGINTLWVGMLFVIRYF 540

RESULT 8
I39295
X-linked PEST-containing transporter - human
C/Species: Homo sapiens (man)
C/Date: 02-Aug-1996 #sequence-revision 02-Aug-1996 #text-change 09-Jul-2004
C/Accession: I39295; I38495
R/Lafreniere, R.G.; Carrel, L.; Willard, H.F.
Hum. Mol. Genet. 3, 1133-1139, 1994
A/Title: A novel transmembrane transporter encoded by the XPC1 gene in Xq13.2.
A/Reference number: I38495; MUID:95072579; PMID:7981683
A/Accession: I39295
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-613 <RES>
A/Cross-references: UNIPROT:P36021; UNIPARC:UP1000012F3CF; EMBL:U05321; NID:g458253; PID
A/Accession: I38495
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 16-613 <RES>
A/Cross-references: UNIPARC:UP1000016A07E; EMBL:U05315; NID:g458246; PIDN:AAB60374.1; P11
A/Gene: XPC1
A/Introns: 218/1; 266/2; 416/3; 464/3; 541/1

Query Match 17.9%; Score 417.5; DB 2; Length 613;
Best Local Similarity 27.5%; Pred. No. 6.7e-21;
Matches 114; Conservative 90; Mismatches 182; Indels 29; Gaps 9;
```

RESULT 9
G69295
oxalate/formate antiporter (oxlf-2) homolog - Archaeoglobus fulgidus
C/Species: Archaeoglobus fulgidus
C/Date: 05-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: G69295
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kitzness, E.F.;
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 354-370, 1997
A/Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Wozniak, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A/Reference number: A69250; PMID:8049343; PMID:9389475
A/Accession: G69295
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1397 <KLE>
A/Cross-references: UNIPROT:Q29880; UNIPARC:UPI0000051135; GB:AE001079; GB:AE000782; NID
C/Superfamily: hypochemical protein c0103

Result 10
P95874
probable transporter protein Smb20272 [imported] - *Sinorhizobium meliloti* (strain 1021)
C:Species: *Sinorhizobium meliloti*
C:Date: 24-Aug-2001 #sequence
C:Accession: P95874
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endod

Query Match	15.8%	Score	368.5;	DB	2;	Length	402;
Best Local Similarity	28.4%	Pred	NO	NO	NO		

RESULT 11

RESULT 11
 T23685
 hypothetical protein M03B6.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T23685
 R:Matthews, J.,
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19782
 A:Accession: T23685
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-596 <WIL>
 A:Cross-References: UNIPROT:Q93896; UNIPARC:UP10000082778; EMBL:Z78545; PIDD:CA01766.1
 A:Experimental source: clone M03B6
 C:Genetics:
 A:Gene: CESP:M03B6.2
 A:Map position: X
 A:Introns: 36/1; 94/1; 273/3; 320/1; 414/3; 533/1

Db 202 IVVVGFFYDSCRAMATGISVAGSGVGTFLVPLICQVCIANLGNOKITWUAWMIFSCVFY 261
 QY 186 GALLRPPSLA-----EDPAVGGR----- 204
 Db 262 GTYRPLPMDLNEIDQEMEPRLQALSKVEDDEDAVESPHNRSSTAASGAIEDEAVS 321
 QY 265 -----AQLTSLHHG----- 214
 Db 322 QNPEVORLSILTEGEGSETPKSDAKKRSHTATRSRKHMTMSNGOHLKLSRGNLS 381
 QY 215 ----- 214
 Db 382 SNRHSRVSARDNOSLSKLSKSGASNTSIAMSGVDPEKFORPMNRKODIFVGGSIQNIK 441
 QY 215 -----PF----- 216
 Db 442 EFKEGTAGYRASTLSIPRSVQAVSQNLNRTGSRILGPGIAEDEBEMIPEFVDGC 501
 QY 217 -----LRYVALTLINT-----GYFPLVLAHLQDLMDPLP 250
 Db 502 CKVLPLPMRNALSEWIDNLKNTMMLICISNLGMMGFYIPMLFKDLESMDLSL 561
 QY 251 AAFLLSVVAISDLVGRVSGMIGDAVPGPVTRLLMLMTTLTGVSALPFAQAAPTALVAL 310
 Db 562 AMFIVPIFGVNTTIGRVFFGWLTDQKLSALTINLILVSGLLTACPLLTSTAGQYFY 621
 QY 311 AVAYGF-----TSGALPLAFSVLPBELIGTRIRYCGILQMIESTIGLLGPP 358
 Db 622 AIVGFIICLKYFFQHLHFAAYICLTSTVADLMGEMLTNSGGLLVVARGIASLVGP 681
 QY 359 LSGVLKRVSGNYTASPVVAGAFLLSGSGLTLTLPHFCFST-----TTSG-----PODLV 408
 Db 682 PACTIVDITGSYDAFVFGGLVTLVAGLISATIP-----FTKKDADTADGMPQLQDDNV 737
 QY 409 TEADITKVPKPKGLEGLNSTSGSPSSQL 439
 Db 738 SCKLSVTERSEALTDYORTISMCKQHOL 768

RESULT 14
 F83484
 Probable MFS transporter PA1286 [imported] - Pseudomonas aeruginosa (strain PA01)
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: F83484
 R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A/Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: F83484
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-399 <STO>
 A/Cross-references: UNIPROT:Q9158; UNIPARC:UPI00000C52EE; GB:AE004558; GB:AE004091; NID
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: PA1286
 C/Superfamily: hypothetical protein c0103

Query Match 12.5%; Score 290.5; DB 2; Length 399;
 Best Local Similarity 29.4%; Pred. No. 1,7e-12;
 Matches 114; Conservative 62; Mismatches 176; Indels 49; Gaps 17;
 QY 16 VVLSAFQSLVGVRSFGVFVEFVAFAFEQAARVSW---IASIGIAVQO---FGSP 68
 Db 8 ILLSCALILALSLGVHGFGLFAPMSADP-----GNGREVFAPALMLQMLVWGLAQP 60
 QY 69 VCSALSTKCGRPVVMGTGILAAQMLLASFATSLTHLYSLIGLSGGMALT-PAPTLA 127
 Db 61 FTGALADRIGARAVLVGGLLYALGLVLMGLSQSASGLSLASGLLIGLSTGTSFVILG 120

QY 128 CLS-CYFSRRSLATGLATVGGLSSFPFAPFOWLLSHYAMRSGLLVSALSLHVACG 186
 Db 121 AVGRAVPEORSMAWGISSAAGSFGQFAMLPOTLIGLIGLMSALLAIGLLVALVPLA 180
 QY 187 ALL--RP-PSLAEDPAGVGPRAQLTSLHHGFELRYVALTLINTGYFIPY--HLVAHL 241
 Db 181 GLMKRPLPPOGHEOSLG--EALREACHSGFWL---LALGFVCGFQVFIQVHLPAVL 235
 QY 242 QDLMDPLPA---AFILSVVAISDLVGRVSGMIGDAVPGPVTRLLMLMTTLTGVSALP 298
 Db 236 VD---QHLPQAVGTTVALVGLFVNVFGYIAGMIGGRMSKP--RLTLTALVLRGVVILF 290
 QY 299 ---PVAQAPTLVLAVALVAGFTSGAL---APLAFSVLPBELIGTRIRYCGILQMIESI 351
 Db 291 LMLPLS-----VYSAAVAFVAMGLMLSTVPLNGVVALTLFGVRNLSMLGIVFLFPHQL 344
 QY 352 GGLGPPISGLYLRVSGNYTASPVVAGAFLLSGSGLTLTLTP 392
 Db 345 GAFLGWLGGVVDRTGSY--DLVMQLSLLSLIALMLNP 383

RESULT 15
 G82445
 Probable oxalate/formate antiporter VCA0554 [imported] - Vibrio cholerae (strain N16961)
 C/Species: Vibrio cholerae
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C/Accession: G82445
 R/Heldelberg, J.F.; Eisen, J.A.; Nelson, M.C.; Clayton, R.A.; Guinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Yamaharan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P. Nature 406, 477-483, 2000
 A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A/Reference number: A82035; MUID:20406833; PMID:10952301
 A/Accession: G82445
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-410 <HEI>
 A/Cross-references: UNIPROT:Q9KM35; UNIPARC:UPI00000C3579; GB:AE004386; GB:AE003853; NID:
 A/Experimental source: serogroup O1, strain N16961; biotype El Tor
 C/Genetics:
 A/Gene: VCA0554
 A/Map position: 2
 C/Superfamily: hypothetical protein c0103

Query Match 12.4%; Score 288; DB 2; Length 410;
 Best Local Similarity 26.9%; Pred. No. 2.6e-12;
 Matches 107; Conservative 70; Mismatches 167; Indels 54; Gaps 14;
 QY 17 VLSAFQSLVGVRSFGVFVEFVAFAFEQAARVSW---WIASIGIAVQOFGSPVSAL 73
 Db 10 ILLAGFCINCLGILVMSVFNKALVDFEWSAADSAPALNTAFSVCLL---VAGIL 66
 QY 74 STFGGPRPVMTGIIAAGMLLASFATSLTHLYSLIGLSGGMALTFAPTLACTS--- 130
 Db 67 QDMGMRNLIIIGTTLTGIMTASGFASSVLMNLTFGWTGAGIGFGY---ACLSPSA 122
 QY 131 ---CYFSRRSLATGLATVGGLSSFPFAPFOWLLSHYAMRSGLLVSALSLHL---VAC 185
 Db 123 MKWFHPSKGMVNGILAAAGFGLAATYLAFLTSLALTLHGLIQTSFMTLGGVLAIAVPLAC 182
 QY 186 GALLRPPS---LAEDPAGVGPRAQLTSL-----HHGFELRYVALT--LTN 227
 Db 183 -TINNPAGYVAEBKLAQGEAKVAVANLSWAKMLKTPQFVALMLMYLAASVGLMI 241
 QY 228 TGYFPLVLAHLQDLMDPLPAFLLSVVAISDLVGRVSGMIGDAVPGPVTRLLMLW 287
 Db 242 IGTNTINIAVOANLPN-----AVYLASIIAIFNSGGRVAAIGLISDKIGG--VRTLLA 292
 QY 288 TTLTGVSALPFAQAAPTALV---ALAVAYGFTSGALAPLAFSVLPBELIGTRIRYCGIG 343
 Db 293 FLLOGGMNVLPATDSEPTLLIGTAIAAVGCG--TLAVFP---SITAEFYGLKRYGNYG 348
 QY 344 LLQMIESTIGLLGPPISGLYLRVSGNYTASPVVAGATL 381

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Db 349 VLYTSGIGCAIGAAVVGYSMTHGGYNLAYTISAAMM 386

Search completed: September 7, 2006, 13:08:03
Job time : 44 secs